

Oy	181	PFETIYUAKSMGLGRFARLRLELOIIOIIRAITSNISVEFSKLSIISTITWTAAG	240
.Db	181	PFETIYUAKSMGLGRFARLRLELRKIIQIIOIYKITSNYSVKLSIYSTWTAAG	240
Oy	241	FIHLVENSDDPWLKGRNSQNIYSFESIYLVMAATSTVGFDDVYAKTSLGRTFIMPTLGS	300
Db	241	FIHLVENSDDPWLKGRNSQNIYSFESIYLVMAATSTVGFDDVYAKTSLGRTFIMPTLGS	300
Oy	301	LILFANVTPENVELFANKRKRTSSYEALKKKFIYVCGNTVDVSATPLANFLRDXSGEI	360
Db	301	LILFANVTPENVELFANKRKRTSSYEALKKKFIYVCGNTVDVSATPLANFLRDXSGEI	360
Oy	361	NTEIYFLGERTPSLELETIFKCYLAATYTFIFSGMSMKMEDJARRAVESAECILIANPLCS	420
Db	361	NTEIYFLGERTPSLELETIFKCYLAATYTFIFSGMSMKMEDJARRAVESAECILIANPLCS	420
Oy	421	DSHAEDISNIRKVLISIKNDSTTRIIIOIIOASHNKVYLPRKIPSMNDTGDNIICFAELKL	480
Db	421	DLHEDDNSNIRKVLISIKNDSTTRIIIOIIOASHNKVYLPRKIPSMNDTGDNIICFAELKL	480
Oy	481	GFIAGGCLVPLCLFPLSLSYEYQKKKMPQTKKHFLLNSMKKKILTORLSDDFAGMSRP	540
Db	481	GFIAGGCLVPLCLFPLSLSYEYQKKKMPQTKKHFLLNSMKKKILTORLSDDFAGMSRP	540
Oy	541	EVARLCFLKMYLILALIEYEKLSLFDGCGILMLPPPOVRIKRTKTLGFFIAETPRKDYRAL	600
Db	541	OYSRLCFKMYLILALIEYEKLSLFDGCGILMLPPPOVRIKRTKTLGFFIAETPRKDYRAL	600
Oy	601	FYCSYCHDVEFIPELITNCGCKSHRSQHTVPSVKRKKCKLKGISSRISGODSPRPVSAS	660
Db	601	FYCSYCHDVEFIPELITNCGCKSHRSQHTVPSVKRKKCKLKGISSRISGODSPRPVSAS	660
Oy	661	T-----SSISNPTTRTILOHDVEDOSDOLDDSSGMHMKPISLDKYTLKRGRKX	709
Db	661	T-----SSISNPTTRTILOHDVEDOSDOLDDSSGMHMKPISLDKYTLKRGRKX	709
Oy	710	YKFRNHIVACYFGDAHSAFMRNFVAPLRASNYTRKELKDIFYIGISLDYLOREMFRLN	769
Db	710	YKFRNHIVACYFGDAHSAFMRNFVAPLRASNYTRKELKDIFYIGISLDYLOREMFRLN	769
Oy	770	FPQIYILPGLCALYSGDLHAANIEQCSKAVLSPPPOSSNQTLVDTPEAIMATLTIGLSLOI	829
Db	770	FPQIYILPGLCALYSGDLHAANIEQCSKAVLSPPPOSSNQTLVDTPEAIMATLTIGLSLOI	829
Oy	830	DSSSPSPSVSEETPRGT-NGHNKSKSCKRVPILTELKNSNIHFLPQGLGEGSLQEN	888
Db	830	DSSSPSPSVSEETPRGT-NGHNKSKSCKRVPILTELKNSNIHFLPQGLGEGSLQEN	888
Oy	889	LHLSTAFSTGTVFSSFLDSLATAFYNYVLELOMLTYGVYSOLOEHLDRDKYGYVA	948
Db	889	LHLSTAFSTGTVFSSFLDSLATAFYNYVLELOMLTYGVYSOLOEHLDRDKYGYVA	948
Oy	949	DSCHLSLSGRKCKLGLSLHEITLSLVNPRNFTFGGLFCGSLDLBGLICVGLYRIIDEE	1006
Db	949	DSCHLSLSGRKCKLGLSLHEITLSLVNPRNFTFGGLFCGSLDLBGLICVGLYRIIDEE	1006
Oy	1009	LNPEKRRVITRIPANEKFLPSDLYVCAIFPFSYACK	1045
Db	1009	LNPEKRRVITRIPANEKFLPSDLYVCAIFPFSYACK	1045
Oy	1014	PSQEHKRFVITRIPSNCHLPLSDLVFCAIFPNTTCK	1050
Db	1014	PSQEHKRFVITRIPSNCHLPLSDLVFCAIFPNTTCK	1050
RESULT	2		
O9T88			
AC	O9T88	PRELIMINARY:	PRT: 1171 AA.
DT	01-MAY-2000 (TREMBlrel. 13, Created)		
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DT	01-MAR-2001 (TREMBlrel. 16, Last annotation update)		
DE	MAXI-K CHANNEL ALPHA SUBUNIT.		
GN	RIBSLOI.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:		

OC Mammalia; Eutheria; Lagomorpha: Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA MEDLINE=98026662; PubMed=9362339;
RX Morita T., Hanaka K., Morales M.M., Montrose-Rafizadeh C.,
RA Guggino W.B. ;
RT "Cloning and characterization of maxi K+ channel alpha-subunit in
RT rabbit kidney.";
RL Am. J. Physiol. 273:F615-F624(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Guggino W.B., Morita T., Hanaka K., Wang S.-X. ;
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
RX EMBL: AF201702; AAF1562.1; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR002052; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003091; -.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: P00169; KCHANNEL.
DR PROSITE: PS00280; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00992; NG_MTASE; UNKNOWN_1.
SQ SEQUENCE 1171 AA; 131673 MW; A3CAAAE635215252 CRC64;

Query Match	41.28%	Score 2359.5	DB 6	Length 1171
Best Local Similarity	42.88%	Pred. No. 1e+160		
Matches 495	Conservative 196	Mismatches 328	Indels 137	Gaps 21

QY	26	AFILISSEVTEFFSSGILLILIFRLILIRMSVK-KK------QIIKGTGILLEFIS	70
Db	24	AFLASMTFFGGLEFI----LMTRLKYLMTVYVCHCGAKAEQKINNSS-----QAD	74
QY	71	GTI-----ANSVRSLHFOGQFHDHIDMLLSAOTFVGQVYLIVFVLSIGSLIYFINS	124
Db	75	GTLLPVDEKEBAVAEEVGMMTSYVDMAAGVIMSACTLGRVLYLVFVLSIGALIVIPIDS	134
QY	125	ADPAGSCSS-VEKDTIPIIDLAFNFFSFSGYGLRPMADDKIKFLEKNSIYDFTIIPPTF	183
Db	135	SNPIESCONFKDDTLOIDMAFNWFLLIYFGLRIIANDKIMLEFVENSIVDEFTVPPVF	194
QY	184	ISYVLKSNMGLRLRALRLLELPLOIOLIRAITSNISVFKSLLSTIILSTWFTAAGFIH	243
Db	195	VSAYLNSWGLRFLRLRLRLOIQLSEIILQFENLILKTSMSIKLYNLSLFIISTWLTAAQFIH	254
QY	244	LVENSGDPWLKGRNSQNIYVFESIYLVMAATTSTYVGCDVAAKTSLGRTFMPTLGSLL	303
Db	255	LVENSGDPWENFQNNQALTEWECYVLLMVTMSTYGVADYAAKTLLGLRPLMVFILGSLAM	314
QY	304	FANITPEVAVELFAKKRYKITSSEYELKGGKFFLYVCGINTVDSYAFNLNPLRDSQGEINTE	363
Db	315	FASYVPEIIEILIGRRKKYGGSYSAVSGRKHLYVCGHITLESVNFLOPLHKORDDVNE	374
QY	364	IVFGEPMPSLEETIFRCYLAATPTFSGAMKWEEDIRAVASEAEACLIITANPLGSDSH	422
Db	375	IVFLHNISPNLELALKRRHFTQVEYFQGSYLVNPHDLARVKIESADACLILANKYCDPPD	434
QY	424	AEDISNIMRYVLSINYNVSTTRIIIOILQOSHUKVYLPKIPSMNMDGTGNIICFALKGFI	483
Db	435	AEDASNIMRYVISIKNYHPKIRIITQMLQIYNNKALLNIPSMNKEGSDGALCLAEKKGFI	494
QY	484	AQSGCLVPGLCTELTSLFEQONKKVMPKQTKMKEHJNSMKKKIILTRLSDPAGAKSPEVA	543
Db	495	AQSLCAGLSLMLNLFESMSFSFIEEDBTQKYYLDEGVSNEMYTEYLSAFVCGLSPTVC	554
QY	544	RUCFLKMYLLLIATLEYKSLSTDEGCGILNPPQVYIRIKNTLGFETIKVDYRRALFYC	603
Db	555	ELCEVKKLKLMLIALEYYSANRES--RLINPQNHKLQIÖEGTLGFLFASDKEVKKRAEYFC	612

Prfam; PF00520; Ion_trans; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SEQUENCE 1151 AA; 128933 MW; 24E62FE0C1D94015 CRC64;

Query Match 41.2%; Score 2357.5; DB 6; Length 1151;
Best Local Similarity 43.2%; Pred. No. 1.4e-160;
Matches 488; Conservative 194; Mismatches 341; Indels 107; Gaps 18;

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QY 15 PKMSC-----TTEIOA-----AFLSSFVTFPFGSLIILIRLIRSVK-KW----- 55
DB 37 PKMDALIIPVMEVPCDSRGORMMWAFPLASSWTFPFGGLFI---LIMRLIKYLMVTCC 92
QY 56 -----OIKGTGIIILEFTSGTI-----ARSHVRSIHPGQGRDHIMLLSAOT 99
DB 93 HCGGKTKRAQKINNGSS-----QADGTILKPYDEKEEAVAAGWMTSVKDMAGVVISQOT 147
QY 100 FVGQVLIVLFVLSIGSLIIFINSADPVGSCSS-YEDKTIPIIDLVFNAFFSFGYGLRFM 158
DB 148 LTGRVLVVLVFLSISGALVIYFIDSSNPDESCQNFYKDFIQLIDMAFNVFLLYGLAFI 207
QY 159 AADKIKFWLENSIVDFTIPPTISYLYKSNWLGRLFLRLRLLELPQIILIRAIKT 218
DB 208 AANDKLMFMLEVNSVYDFEYVPPVSVYLNRSWGLRFLRLRIQFSEILOFLNLIK 267
QY 219 SNSVFSKLLSIIISTWTFAGFIHLVENSQDPMILKGRNSQISYFESYLYVMATTSYVG 278
DB 268 SNSIKLVNLSIFSTWTLAAGFIHLVENSQDPMENFQNNALTYWECVYLLMVTMSYVG 327
QY 279 FGDVVAKTSLSGTFIMFTLGLSLIFANVYIPMEVLFANKRKRYTSYELAKGKFIYVCG 338
DB 328 YGDYAKTTLGLRFVFFIILGLAMFASYVPEIILGNKKYGGSYSAVSRRKIIVCG 387
QY 339 NITVDVTAFLNPLRDSGELIIVELEGETPSLELETIFKCYLAATYFISGAMKWE 398
DB 388 HTLESVGNFLKDFLHKRDQVNVFVLFHNSPMLLEALFKRHFTQVEYFQGSVLNPH 447
QY 399 DLRAVAASAELCLIANPLCSDSAEDISNMRVLSKNDSTRIITQIILQSNKYLL 458
DB 448 DLARKISSADACLILANKYCADPDAEDASINMRVYSIKNHPKIRITOMLOYNKAKHL 507
QY 459 PRIPSMNDGTGNICFPAELKLGFTAGGLVGLCTPLTSLFVEQNKVMPQOTMKKHL 518
DB 508 LNIPSMNKEGDDAICLAELKIGFTAGSLAGSLTMLANLFMSMFIKIEDTQOKYLL 567
QY 519 NSMKKILITQLRSDFAQMSPEVARLCLFKYLLLIILAEKYSLETFDGCGLIILNPPOV 578
DB 568 EGVSNEMYTEYLSSAFVGLSFTVCELFCVKLKLIMAIKYSANRES--RILINPKNHL 625
QY 579 RIRKNTLGFIAETPKDVRALFYCSVCHDVFIPELITNCGCKRSRQNHITVPSVKRK 638
DB 626 KIOETGLFFIASDAKEKRAFFYKACHDITDPKRIKCCCK--RIEDRQPSLSPK 682
QY 639 KCLKISIRISIGQDAP-----PRVASTSISNFTTRTLQDVQDSDQLDSSGMFHC 692
DB 663 KKGKRGKRNSSNSPKLMRHPPLIPGNDQIDN-----MDSNKKYDSTGMFHC 733
QY 693 KPTSLDKVTLKRTGSKYKFRNHIVACYFGDAHSAFPGMLRNFVMDLRASNYTRKELDIV 752
DB 734 APKEIEKIVILTRSEAAAFVLSGHVYVVCIFGDVSSALIGLRNLMPLRASNFIYHELKHLV 793
QY 753 FTGSLDYLOREKRLRNPQIYILPGCALYSGDLAAANEQCSMCANVLSPPQPSNQT 812
DB 794 FVGSLLEYLKRREKTLNHPKVSILPGTPLSRADLRVNNICDMKVILSANONNIDVSL 853
QY 813 VDETAIMATLTIGSLQID-----SSDPSPSVSE-ETPGYTGCHN 851
DB 854 QDKCEILASLNKSMQFDSIGVLOANSQFTPPGMDRSSPNSVYHGLRPPSTTTGCVN 913
QY 854 EKSNCRKVPILTCLNPSNIHFIQDLGLEGSLQETNHLHLSAFSTGTVFSSFLDLSLA 911
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DB 914 -----IPITTELVNDTNVOFLQ---DDDDPDPTELYLTOPFACGTAFAVSLDLSMS 963
QY 912 TAFVNYHYVLELLOWLVGGSQLEQHLDKDKYGVADSCSTLSGRNRCKLGLSLHET 971
DB 964 ATYFNDNITLIRLLVYTGATPELEALIAENALRGYSTPOTLANRRCRAOALALD 1023
QY 972 ILSDVNPRNTFGOLFQCSGLDFGLCVGLYRIIDEELNPE--NKRFTYTPRANFKLLP 1029
DB 1024 PPAADGGDCGCGDLECKALKTKYNNMCFGIYRLRDAHLSTPQCGTKRYVITNPPYEFELVP 1083
QY 1030 SDLVCAIPESTACKRNEEFSLOKSYETVKNASQTTDTRHKLISSPL 1079
DB 1084 TDLIFCLMQF-----DHNAGQSRASLSHSSSHSSQSSSKSSSVHSI 1124
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RESULT 6
ID Q12921 PRELIMINARY; PRT; 1154 AA.
AC Q12921;
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DE 01-OCT-2000 (TREMUREL. 15, Last annotation update)
DE CALCIUM ACTIVATED POTASSIUM CHANNEL.
GN HSLQ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95085775; PubMed=7993625;
RT Tseng-Crank J., Foster C., Mertz R., Godinot N., Reinhardt P.;
RT "Cloning, expression, and distribution of functionally distinct
RT Ca(2+)-activated K+ channel isoforms from human brain.";
RL Neuron 13:1315-1330(1996).
DR EMBL; U11717; AAC50353.1; -.
DR InterPro; IPR000636; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR002052; -.
DR InterPro; IPR003006; -.
DR Pfam; PF00520; Ion_trans; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SEQUENCE 1154 AA; 129231 MW; 22C4DB64BC251D51 CRC64;
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Query Match 41.2%; Score 2356.5; DB 4; Length 1154;
Best Local Similarity 43.2%; Pred. No. 1.7e-160;
Matches 488; Conservative 193; Mismatches 342; Indels 107; Gaps 18;

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QY 15 PKMSC-----TTEIOA-----AFLSSFVTFPFGSLIILIRLIRSVK-KW----- 55
DB 37 PKMDALIIPVMEVPCDSRGORMMWAFPLASSWTFPFGGLFI---LIMRLIKYLMVTCC 95
QY 56 -----OIKGTGIIILEFTSGTI-----ARSHVRSIHPGQGRDHIMLLSAOT 99
DB 96 HCGGKTKRAQKINNGSS-----QADGTILKPYDEKEEAVAAGWMTSVKDMAGVVISQOT 150
QY 100 FVGQVLIVLFVLSIGSLIIFINSADPVGSCSS-YEDKTIPIIDLVFNAFFSFGYGLRFM 158
DB 151 LTGRVLVVLVFLSISGALVIYFIDSSNPDESCQNFYKDFIQLIDMAFNVFLLYGLAFI 210
QY 159 AADKIKFWLENSIVDFTIPPTISYLYKSNWLGRLFLRLRLLELPQIILIRAIKT 218
DB 211 AANDKLMFMLEVNSVYDFEYVPPVSVYLNRSWGLRFLRLRIQFSEILOFLNLIK 270
QY 219 SNSVFSKLLSIIISTWTFAGFIHLVENSQDPMILKGRNSQISYFESYLYVMATTSYVG 278
DB 271 SNSIKLVNLSIFSTWTLAAGFIHLVENSQDPMENFQNNALTYWECVYLLMVTMSYVG 330
QY 279 FGDVVAKTSLSGTFIMFTLGLSLIFANVYIPMEVLFANKRKRYTSYELAKGKFIYVCG 338
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Db 331 YGVYVATTTGRLFMVEFLLGGLAMFASVYPELLELIGNRKKKGGSSAVSGRKHIVCG 390
Qy 339 NITVDVYAFARLNRDLRDKSGEINTEIVELGETPSPLELETFKCYLAATTFFISGSAMKE 398
Db 391 HITLESYVNLKDFLHKDRDQVNEIVFLNHSINPLELEALFKRHFPQVEVYQGSVLPNH 450
Qy 399 DLRAVAVESAACLIINPLCSHAEISIMRVLSIKYNDSTTRIIIOLOSCHKVYL 458
Db 451 DLARVKIESADACILINKKCADPADASINIMRVISIKNHPKIRITOTLOLYHNKAHL 510
Qy 459 PKIRSMNMDGDNICFAELKGLFIAOGCLVPGCTFLTSLFVBNKVMKPKQWKKHFL 518
Db 511 LNPDSNMKEEDDAICLAELKGLFIAOSCLAOGSLTMLANLFSMRSTIKIEEDWQVYL 570
Qy 519 NSMKNKILTORLSDDFAGMSFPEVARLCFLKMYLLLAIEYKSLFTDGFGLILNPPQV 578
Db 571 EGVSENEYTEVLSAFAVGLSPYVCELCFVKLKLMAIEYKSNRBS--RIILNPGNHL 628
Qy 579 RIRKNTIGFFIAETPKVRRALFYCSCHDDVFLPELITNCGCKSRROHTVPSVYKRM 638
Db 629 KIOGTLGFFIASDAKEVKRAFFCKACHDDITDPKRIKCGCK--RLDEQDPSLSPK 685
Qy 639 KCLGISRSISGQDSP-----PRVSASTSSISNFTRTLQHDVEQDSDOLDSGFMFHC 692
Db 686 KKGNGGMRNSPNTSPKLMRHPDLIFGNDQIDMDSHVKKY-----DSTGMFHC 736
Qy 693 KPTSLDRVTLKRTGSKYKFRNHIVACVFGDASHAPGLRNFVPLRASNYTRKELDIY 752
Db 737 APRKEIKYILTRSEAAMTVLSGHVYVCIFGDVSSALIGRLNVLPRASNPHYHELKHIV 796
Qy 753 FVIGSLDLOVRMRLRNPQOYIILPGCALYSGDLHAANIECCSMCVLSPPPQSSQTL 812
Db 797 FVGSIEYLKREMETLMEPKVSLPGTPLSRADLRANINLCDCVYLISANONNIDTSL 856
Qy 813 VDTFAINATLIGSLQID-----SSSDPSPSYSE--ETPGYTNCHN 851
Db 857 QDKKCIASLNKIKMOPDDISGVLQANSQGTTPRGMDRSSPDNSPVHGLMRQPIITTCVN 916
Qy 852 EKSCKRVPILTELKNSNIHFIBOLGLEGSLQETLNLHLSSTGTGVSSFLDLSLA 911
Db 917 -----IPITTELNDNTNOFLDQ---DDDDDPDTLEYLTOPACGTAFVSVLDLSMS 966
Qy 912 TAFVNVYVELLOMLVTVGVSQSOEHLDKDKYGVADSCSLISGNNRCLGILLSHER 971
Db 967 ATYFNDNITLIRTVLGGARPELEALIAEENALRGYSTPOTLANDRCVQALALDQ 1026
Qy 972 ILSDVNRNFTFGQLFCGSLDFGILCVGLYRIIDEELNPE--NKRPVITPRANEFKLLP 1029
Db 1027 PFALDGGGGCGDLFCALAKTYNMLFCGYIRLRAHLSTPSQCTKRYVITNPREFELVP 1086
Qy 1030 SDLVFCAIPSTACVYKRNNEFSLOKSEIYVKNASQTTEDFRHKLSSHPL 1079
Db 1087 TDLIFCLMOF-----DHNAGOSRASLSHSSSSQSSSKSSVHSI 1127

RESULT 7
Q9UBB0 PRELIMINARY; PRT: 1154 AA.
AC Q9UBB0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CALCULUM-ACTIVATED POTASSIUM CHANNEL ALPHA SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LENS EPITHELIUM;
RA Rae J.L., Shepard A.R.;
RT Identification of potassium channels in human lens epithelium.;
RL (in) Civan M.M. (eds.);

RL Current topics in membranes. The eye's aqueous humor - from secretion
RL to glaucoma, pp.45:69-104, Academic Press, San Diego (1998).
DR EMBL: AF025999; AAB88802.1; -
DR InterPro: IPR000636; -
DR InterPro: IPR001623; -
DR InterPro: IPR002052; -
DR InterPro: IPR003066; -
DR InterPro: IPR003091; -
DR Pfam: PF00520; Ion_trans. 1.
DR PRINTS: PR00169; CHANNEL.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MFase; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1154 AA; 129208 MM; 621F18A4DE7BD274 CRC64;

Query Match 41.2%; Score 2356.5; DB 4; Length 1154;
Best Local Similarity 42.9%; Pred. NO. 1.7e-160;
Matches 487; Conservative 197; Mismatches 333; Indels 119; Gaps 19;

Qy 15 PKMSC-----TTEIOA-----AFILSFYFFESGLIILFRLIMRSVK-KW---- 55
Db 40 PKMDALLIPTMEVPCDSRGQRMMAFLASSMYTFEGGLFII---LMTKTKLMTVCC 95
Qy 56 -----QIIKGTGIIIEFTSGTI-----ARSHVSLHFQGFPHIEMLSAQT 99
Db 96 HCGGKTEAQRKINNSS-----QADGTLKPVDEKEEVAAEVGMWTSQWAGVMSAQT 150
Qy 100 FVGQVILVFLVSLIGSLIIFYINSADPVGCS--YEADKTIPLDVNAFESFYGRLFM 158
Db 151 LTGRLVVLVFLALSTGLVLYFIYDSSNPISCONFYDFLOIDMAPNVFLYFGRLFI 210
Qy 159 AADKIKFWEIEMNSYDIETIPTFTISYLYKSNMGLRFLRALRLLELPOLILRAKT 218
Db 211 AANDKLMFWEIVANSVDVFTVPVFAVSUYLNRSLGRLFRALRLLOFSEILOFLNLT 270
Qy 219 SNSVKFSLKLSIILSTFTAGFTAGFTIHYENSGDPLKRNQNSNISPESTILVMAATSTVG 278
Db 271 SNSIKLVNLSTFTSTVLTAAGFTIHYENSGDPEPNFONNOLATVWCYVLLVMTYSTVG 330
Qy 279 FGDVAVTSGLRTEIMFTTGLSLILFANYIPEWELEFANKRYTSYEALAKKFTVCG 338
Db 331 YGVYVATTTGRLFMVEFLLGGLAMFASVYPELLELIGNRKKKGGSSAVSGRKHIVCG 390
Qy 399 DLRAVAVESAACLIINPLCSHAEISIMRVLSIKYNDSTTRIIIOLOSCHKVYL 458
Db 451 DLARVKIESADACILINKKCADPADASINIMRVISIKNHPKIRITOTLOLYHNKAHL 510
Qy 459 PKIRSMNMDGDNICFAELKGLFIAOGCLVPGCTFLTSLFVBNKVMKPKQWKKHFL 518
Db 511 LNPDSNMKEEDDAICLAELKGLFIAOSCLAOGSLTMLANLFSMRSTIKIEEDWQVYL 570
Qy 519 NSMKNKILTORLSDDFAGMSFPEVARLCFLKMYLLLAIEYKSLFTDGFGLILNPPQV 578
Db 571 EGVSENEYTEVLSAFAVGLSPYVCELCFVKLKLMAIEYKSNRBS--RIILNPGNHL 628
Qy 579 RIRKNTIGFFIAETPKVRRALFYCSCHDDVFLPELITNCGCKSRROHTVPSVYKRM 638
Db 629 KIOGTLGFFIASDAKEVKRAFFCKACHDDITDPKRIKCGCK--RLDEQDPSLSPK 685
Qy 639 KCLGISRSISGQDSP-----PRVSASTSSISNFTRTLQHDVEQDSDOLDSGFMFHC 692
Db 686 KKGNGGMRNSP-----NTSPKLMRHPDLIFGNDQIDMDSHVKKYDST 730
Qy 687 GPFHMKPTSLDKVTLKRTGSKYKFRNHIVACVFGDASHAPGLRNFVPLRASNYTRK 746
Db 731 GPFHMKAPKEIKYILTRSEAAMTVLSGHVYVCIFGDVSSALIGRLNVLPRASNPHYH 790
Qy 747 ELKDIVTIGSLDYLQREWRRLRNPQOYIILPGCALYSGDLHAANIECCSMCVLSPPP 806

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Db 791 ELKHIVFGSIEYLKREMBETLHNFPEKYSILPOTPLSRADLRVAINLDCMVCYILSANQNN 850
Oy 807 SSNOQLVTEAIMATLTGSLQID-----SSSPSPSVSE-ETPG 845
Db 851 IDDTSLQDKECILASLNKSMQFDDISIGVLQANSOGFTPPGMDRSSPNSPVHGLRQPS 910
Oy 846 YTNNGNEKSNCRKVPILTELKNPNSIHFIHQGLGSLQETNLHLSTAFSGTFFSSSF 905
Db 911 ITTGVN-----IPITELVNDINVOFLDQ---DDDDDPTELYLTQPFACGTAFAVS 960
Oy 906 LDSLATAFYNYHYVLELQMLVTGVSQLEQHLDKRVYGVADSCSTLSGRNCKLGL 965
Db 961 LDSLMSATYFNDILTLRLTYTGATPELEALINAEINALGCGYSTPQTIANRDCRAVQ 1020
Oy 966 LSLHETILSDVNPRTFQGLFCGSLDLFGILCVGLYRIIDEELNPE--NKRFTVITRAN 1023
Db 1021 LALDGPADLDGCGCYDLCFKALKTYNMLCFGIYRLRDAHLSTPSCOTKRYVITNPPY 1080
Oy 1024 EFKILPSDLVFCALPFSNACYKRNEEFLQKSYELVNKASQTEDETFPHKLSSHPL 1079
Db 1081 EPELVPTDLIFCLMOP-----DHNAQOSRASLSHSHSSOSSSKSSSVHSI 1127

RESULT 8
O12960 PRELIMINARY: PRT: 1178 AA.
AC O12960
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE LAGE-CONDUCTANCE CALCIUM-ACTIVATED POTASSIUM CHANNEL.
GN HSGO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBSTANTIA NIGRA BRAIN TISSUE;
RA Dwojereky S.I., Trojnecki J.T., Gridboff V.K.;
RT "Cloning and expression of a human large-conductance calcium-activated
RT potassium channel."
RL Brain Res. Mol. Brain Res. 27:189-193(1994).
RM [2]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBSTANTIA NIGRA BRAIN TISSUE;
RA MEDLINE=9318148; PubMed=7687074;
RA Butler A., Tsunoda S., McCobb D.P., Wei A., Salikoff L.;
RT "mlo, a complex mouse gene encoding 'maxi' calcium-activated
RT potassium channels."
RL Science 261:221-224(1993).
DR EMBL: U13913; AA85104.1; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR002052; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00520; Ion_Ctrans; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SO SEQUENCE 1178 AA: 131026 MW: 4F00800A725948B2 CRC64;
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Query Match 41.2%; Score 2356.5; DB 4; Length 1178;
Best Local Similarity 42.9%; Pred. No. 1.7e-160;
Matches 487; Conservative 197; Mismatches 333; Indels 119; Gaps 19;

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Oy 15 PKMSC-----TTEIDA-----AFILSSVTFEFGSILILIRLLIRLSRK-KW----- 55
Db 64 PKMDALITPVMEVPCDSRGORMMWAFILASSKVFEGGLEFI---LIMRLKLYIMTVCC 119
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Oy 56 -----QIKGTGIILETSGTI-----ARSHVRSILHFGOGFRDHIEMLSAQT 99
Db 120 HCGGKTRKAOQKINMGSS-----QADGTLKPYDEKEEAAYAEVGMWTSVKDNAGVWISAO 174
Oy 100 FVGQVLYLVLEVLVSGSLIIVFINSADPVGSSS-YEDKTIPIDLVFNAPFSFGYGLRFM 158
Db 175 LTGRVLYLVLEVLVSGSLIIVFINSADPVGSSS-YEDKTIPIDLVFNAPFSFGYGLRFM 158
Oy 159 AADKIKVLEWENSLVDITPTPTFIISYLYKSNMGLRFLRALRLLELPOLQILRAIKT 218
Db 235 AANDKLMFMLEVNSVVDFTVPVFSVYLRNSWGLRFLRALRLRLOPSEILOFINILKT 294
Oy 219 SNSVFKSLSTIISTWTAGTILVENSQDPMVLKGNNSONISFEESIYVMAFTTVG 278
Db 235 SNSIKLVNLISFISTWLTAGTILVENSQDPMVFNONALTYWECVYLLMWTMTVG 354
Oy 279 FGDVVAKTSIGRTFIMPTLGLSLIFANVYIDEMVELFANKRKYSSYBALGKFTIVCG 338
Db 355 YGDVYAKTTLGRLFVVFITLGLAMFASYPEIIEILGNRRKYGSGYSVAGRKHIYVCG 414
Oy 339 NITDVSATFLRNFLRDKSGEINTEIYVFLGETPPSLEETIFKCYLATYTTISGAMKE 398
Db 415 HITLESVSNFLKDFLHKRDVDVNEIVFLNHSPLLEALFKRHFTQVEFYQSVLNP 474
Oy 399 DLRRVASEAEACLTIANPLCSDSHAEDISNIMRYLSIKNDSTRTITIOLOSHNKVYL 458
Db 475 DLARKIESADCLLAKKACADPAEDASNIMRYLSIKNDSTRTITITOMLOTHNKVYL 534
Oy 459 PKIPSMNDTSDNIIICFALKLGFLAQGLVPGTFLTSLFVEBONKVMKPTKKHFL 518
Db 535 LNIPSMNKEGDALCLALNELKLGFLAQGLVPGTFLTSLFVEBONKVMKPTKKHFL 518
Oy 519 NSMKKILTORISDDFAKMSPEVARLCLFKNYLLILIEKSLFTDQFCGLILNPPQV 578
Db 595 EGVSNEMYTEVLSAFVGLSEPTVCELCFVKLMLMIEKKSANRES--RLILNPVHNL 652
Oy 579 RIRKNTLGFIAEPKVDRLRFLCYSCVDVFPDELITNCGCKSRSONHTVPSVKRMK 638
Db 653 KIQEGTLOFLFASDAKEVKRAFFYCKACHDITDPKRIKKCGCK--RLDEQPSYLSPK 709
Oy 639 KCLKGISRISGQDPPPVASSTSSISNFTRTLOHD-----VBQDSQDQDLS 686
Db 710 K-----KORNGGMKNSP-----WTSPLKMRHDDLIPGNDQIDNMSVKKYDST 754
Oy 687 GMFHWCKPTSLDKVYLAKTKGSKYKFRNHVYACVFGDAHSAPMGLRNVPMLRASNYTRK 746
Db 755 GMFHWCAPEKEIKVILTRSELAAMTVLSGHVYVCIFGVDSALIGLRNLYMPLRASNFHYH 814
Oy 747 ELKQIVFGSLDYLOREKRFNRNPOIYILPGCALSGDLAANAEOGSCMAVLSPPPO 806
Db 815 ELKHIVFGSIEYLKREMBETLHNFPEKYSILPOTPLSRADLRVAINLDCMVCYILSANQNN 874
Oy 807 SSNOQLVTEAIMATLTGSLQID-----SSSPSPSVSE-ETPG 845
Db 875 IDDTSLQDKECILASLNKSMQFDDISIGVLQANSOGFTPPGMDRSSPNSPVHGLRQPS 934
Oy 846 YTNNGNEKSNCRKVPILTELKNPNSIHFIHQGLGSLQETNLHLSTAFSGTFFSSSF 905
Db 935 ITTGVN-----IPITELVNDINVOFLDQ---DDDDDPTELYLTQPFACGTAFAVS 984
Oy 906 LDSLATAFYNYHYVLELQMLVTGVSQLEQHLDKRVYGVADSCSTLSGRNCKLGL 965
Db 961 LDSLMSATYFNDILTLRLTYTGATPELEALINAEINALGCGYSTPQTIANRDCRAVQ 1044
Oy 966 LSLHETILSDVNPRTFQGLFCGSLDLFGILCVGLYRIIDEELNPE--NKRFTVITRAN 1023
Db 1021 LALDGPADLDGCGCYDLCFKALKTYNMLCFGIYRLRDAHLSTPSCOTKRYVITNPPY 1104
Oy 1024 EFKILPSDLVFCALPFSNACYKRNEEFLQKSYELVNKASQTEDETFPHKLSSHPL 1079
Db 1105 EPELVPTDLIFCLMOP-----DHNAQOSRASLSHSHSSOSSSKSSSVHSI 1151
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RESULT 9
013150 PRELIMINARY; PRT: 1178 AA.
AC 013150;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL.
GN HSL0.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND, AND UMBILICAL SMOOTH MUSCLE;
RX MEDLINE=96024676; PubMed=7573516;
RA McCobb D.P., Fowler N.L., Featherstone T., Linggle C.J., Salto M.,
RT Krause J.E., Salkoff L.;
RT "A human calcium-activated potassium channel gene expressed in
RT vascular smooth muscle.";
RT Am. J. Physiol. 269:H767-H777(1995).
DR EMBL: U23767; AAA92290.1; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR002052; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00520; Ion_trans; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1178 AA; 130998 MW; AD3C9634F8A21EEC CRC64;

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Query Match 41.2%; Score 2356.5; DB 4; Length 1178;
Best Local Similarity 42.9%; Pred. No. 1,7e-160;
Matches 487; Conservative 197; Mismatches 333; Indels 119; Gaps 19;

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15 PKMSC-----TTEIOA-----AFLLSFTVFGSLILLIRLIRSVK-KW-----55
64 PKMDALIPVMEVPDPSRQGMMAFLASSMTVFGLFI-----LLMPTLKLMTVCC 119
56 -----QIKGTGILELFTSGT-----ARSHVRLHOGQFRDIEMLLSQOT 99
120 HCGGKTEAOIKNGSS-----QADGTLKPYDEKEEAFAAEVGMTSVKAGVMISQOT 174
100 FVGQVILVLEVLISGLIITYFINSADPVGSCSS-YEDKTPIDLVFNAPFSFGLEFEM 158
175 LTGVLVVLVVALSIGALVITYFIDSSNPDESCQNFYKDFIQIDMAFVVFLLYFGLRFI 234
159 AADKIKFWLEMSIVDIETTPPTFISYLYKSNWLGFLRALRLLELQIILRAIKT 218
235 AANKIKFWLEMSIVDIETTPPTFISYLYKSNWLGFLRALRLLELQIILRAIKT 218
219 SNSKFKSLIILSTWFTAGFTHLVENSGDPLKGNNSINISYFESIYVMAITSVG 278
295 SNSIKLVNLSIFSTWFTAGFTHLVENSGDPLKGNNSINISYFESIYVMAITSVG 278
279 FGDVAKTSIGRTFIMEFTLGLSLILFANYIPENWELFANKKRTSYSEALGKKFIYVCG 338
355 YGDVAKTSIGRTFIMEFTLGLSLILFANYIPENWELFANKKRTSYSEALGKKFIYVCG 338
339 NITVDSYAFALRNFLRDKSGEINTEIFLGTTPPSLEETIFKCYLAATYTFISGSANKWE 398
415 HITLESVNFPLKDFLHKORDVDVEIFVNLHNSPDLLEALFKRHPFOVEYQGSVLPNH 474
399 DLRAVAVESAFACILIANPLCSDSHADISIMAVLSKANDSTTRIIILQLOSHNKVYL 458
475 DLRAVAVESAFACILIANPLCSDSHADISIMAVLSKANDSTTRIIILQLOSHNKVYL 458
459 PKIRSMMDNGDNIITCAELKGLFIAGCIVPGCTFETLSFVSONKVMKPKOMKKHFL 518
535 LNTFSNMKESGDDAICLAELKGLFIAGCIVPGCTFETLSFVSONKVMKPKOMKKHFL 518

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OY 519 NSMKKILTORLSDDFAGMSPEVARLCFLMYLLIAIEYKSLFTDGFCLILNPPQV 578
DB 595 EGVSNEMYTEYLSAFVGLSEPTVCELCFVKLKLIMAIEXKANRES--RLINPGNHL 652
OY 579 RIRKNTLGFIAEPKQVRLALFYCSVCHDVFIPELITNCGCKSRSGHTIVSVKRMK 638
DB 653 KIQEGTLEFFIASPAKKEKRAFFCKACHDITDPKRIKCGCK--RLEDEQSTLSPK 709
OY 639 KCLGISIRISGODSPPVASSTSSISNFTTRLOHD-----VEQDSDQLDSS 686
DB 710 K-----KRNKGMSNRP-----NTSPKLRHDPDLLPGNDQIDNMSNVKAKDST 754
OY 687 GMEHCKPTSLDKVTLKRTGSKYFRNHVYACVFGAHSAPMGIRNFMPLRASNTTRK 746
DB 755 GMEHCKPTSLDKVTLKRTGSKYFRNHVYACVFGAHSAPMGIRNFMPLRASNTTRK 746
OY 747 ELKIDVIFGSLDYLOREHRLRNFPQIYILGCLALSYSDLAANEGCSMCVAVLSPRPQ 806
DB 815 ELKHIVFGSLDYLOREHRLRNFPQIYILGCLALSYSDLAANEGCSMCVAVLSPRPQ 806
OY 807 SSNOTLVDTFAIMATLTGSLQID-----SSDPSPSVSE-ETPG 845
DB 875 IDDTSLQDKCEILASLNKSMQFDDSGVLOANSOGFTPPGMDSSPDNSPVHGMLOPS 934
OY 846 YTNHNEKSNCRKVPILTELKPNINHEFTEQLGLESLOETNHLSTASTGTGVSSSF 905
DB 935 ITTGVN-----IPITELVNDTNVOFLDQ-----DDDDDPTELYLQPFACGAFVAVS 984
OY 906 LDSILATFVYVHYVLELLOMAYTGGVSQLDQHLDDKKVYVAVASCSLISGRNRCKGL 965
DB 985 LDSILATFVYVHYVLELLOMAYTGGVSQLDQHLDDKKVYVAVASCSLISGRNRCKGL 965
OY 966 LSLHETILSDVNPNNFEGOLFCGSLDLFGILCVGLYRIIDEELNPE--NKRFTYTPAN 1023
DB 1045 LALLDGPRAIDGDCGCGDLFCRKLKTYNMLCFGIRLRADHLSTPSCQTRRYIYTPY 1104
OY 1024 EFKLLPSDLVCAIPFSTACYKRNEEFSLOKSYEVINKASQTTEDTRHKLSSHPL 1079
DB 1105 EFKLLPSDLVCAIPFSTACYKRNEEFSLOKSYEVINKASQTTEDTRHKLSSHPL 1079
RESULT 10
012917 PRELIMINARY; PRT: 1113 AA.
AC 012917;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE CALCIUM DEPENDENT POTASSIUM CHANNEL ALPHA SUBUNIT.
GN MAXIK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MYOMETRIUM;
RX MEDLINE=96196569; PubMed=8612769;
RA Meera P., Wallner M., Jiang Z., Toro L.;
RT "A calcium switch for the functional coupling between alpha (hslo) and
RT beta subunits (KV/calpha beta) of maxi K channels.";
RT FEBS Lett. 382:84-88(1996).
RL EMBL: U11058; AAB65837.1; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR002052; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00520; Ion_trans; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1113 AA; 125210 MW; ID9A857F69106CE8 CRC64;

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Query Match 41.2%; Score 2355.5; DB 4; Length 1113;
Best Local Similarity 43.4%; Pred. No. 1.9e-160;
Matches 482; Conservative 196; Mismatches 328; Indels 105; Gaps 17;

QY 26 AFILSFTFFSGILILIFRLIRSVK-KW-----QIIKGTGIIILEFTS 70
DB 24 AFLASSWVTFEGGLFIT-----LMRLTKYLMVTVCCHCGKTKKAKINNGSS-----QAD 74

QY 71 GTI-----ARSHVRLHFOGQFRDHIEMLSAQTFGVQVLYLVFLVSLIGSLIYFINS 124
DB 75 GTLKPVDKEEAAVAEYGMWTSVKDMAGVMISAOTLTGRVLYLVFLVSLIGALVIYFIDS 134

QY 125 ADPPGSSS-YEDKTIPIDLVFNAFESFYGLRPMADDKIKFLEMNSIVDITIPTE 183
DB 135 SNPIESCONFKDFTLQIDMAFNFFLLYFGLRIANDKIMFLEVNSVDFETVPVF 194

QY 184 ISYLLKSNMGLRLRLRLRLLELPQIILRAIKTSNSVSKSLSTIILSTWTFPAAGFIH 243
DB 195 VSVYLNRSWGLRLRLRLRLQFSEILQFLNLIKTSIKLVNLSIFISWTLAAGFIH 254

QY 244 LVNSGDPWLKGRNSQNSYFESIYLVWATTSTVGFDVYAKTSLGRFTIMEFTLGLSL 303
DB 255 LVNSGDPWENFQNNQALTYMECYLLMTVMTSTVGQDVYAKTTLGRLEWVFILGLIAM 314

QY 304 FANIPPEWELFANKRKYTSSEYALKGKFFLYVCGNTVDSVTFALNRLFLDKSGEINTE 363
DB 315 FASVPEIETELIGNRKKYGGSYSAVSGRKLIVYCGHTLLESVSNFLDFLKRDQDVAVE 374

QY 364 IVFLGETPPSLEETIFKCYLAATYTFISGAMKEDLRVAVESAECILIANPLCSDSH 423
DB 375 IVFLHNISPDELEALFKRHFTQVEFYOGSVLNPHDLARVKIESADACLIANKYCADPD 434

QY 424 AEDISNTRVLSINVDSTRIIILQIASHNKVYLPIKPSNMWTDGNIITCEALKIGFI 483
DB 435 AEDASNTRVLSINVKHPKIRIITQMLQYHNKALHNPISNMKEGDALICLALKIGFI 494

QY 484 AOGGLVGLCFLTSLVEONKKVMPKOTWKKHFLNSKNNILQRLSDDFGASPEVA 543
DB 495 AOGSLAOGSLTMLNLSMKSFKIEBEDTMOKYLEGVSNEMTYEYSSAFVGLSFPFVC 554

QY 544 RLCEFLKMYLLILIAIEYKSLFTDGCGLILNPPQVRIKNTLGEFIETPRVRALEYC 603
DB 555 ELCEVKLKLMIAIEYKSANRES--RLINPQNLKIQEGTLGFIASDAKEVRAFEYC 612

QY 604 SVCHDDVPIPELITNCCKSKRSRQHTVPSVKRKKCLGKISSKISGODSPRVSASISS 663
DB 613 KACHDDITDPRIKRCGCK--RLDEQPSLSPRK-----KORNGGRNSP----- 656

QY 664 ISNFTTTLQHD-----VEDSDQLDSSGMFHWCKPSTLQDKVTLKRTGSKSKYK 711
DB 657 --NTPSKLMDPLILIGENDQIDNMDSNVKKYDSTIGMHCAPKEIEVILTRSEAAATV 714

QY 712 FRNHIVACVFGDAHSAPWGLNFPYPLRASNYTRKELDIYFISGLDYLOREMFRLNFP 771
DB 715 LSGHVAVVICBEDVASALIGLNLVMPRLASNFHYHELKHIVFVGSIEVLRKEMELIHNFP 774

QY 772 QIYLLPGCALYSGDLHAANIEQCSKCAVLSPPOSSNQTLVDEALMATLTJISLQID- 830
DB 775 KVSILPGPLSRADLRANVIMLCMVCVILSANQNNIDTSLQDEKICLASINIKSMOPDD 834

QY 831 -----SSSDPSPSVSE-ETPGYTNHGHKESKCRVPLITELKNSN 870
DB 835 SIGVLQANSOGFTPPGMDRSSPNSPVHGMRLQPSITTVGN-----IPITTELVDJTN 887

QY 871 IHFEIQLGLEGSLQETNLHLSAFTSTCTVSSSFLDLSLTAAYNVHLLQMLVYGC 930
DB 888 VQFLDQ---DDDDPDTFLYLTQFPACCTAFAVSLDLSMATYFNDIILTLITLVYGG 944

QY 931 VSSOLEHLDKDKYGVADSCSTLSLGRNCKLGLLSHETILSDVNRNTEFGOLFCGSL 990
DB 945 ATPLELIALIEENMLRGYSTPOTLANHRCRVAQLALLDGPFDLGGCGYDLFCAL 1004

QY 991 DLRCGLCVGLYRITDEEELNPE--NKRFTVTRPANEKLLPSDLVPCALFPSTACYRNE 1048
DB 1005 KTYMMLCFGYIRLDAHLSPSQCCKRYVTNPEYELVPTDILFCMLQF----- 1055

QY 1049 EFSLOKSYEIVNKASQTTEDTFRHLKSSHPL 1079
DB 1056 DHMAGOSRALSHSHSSHQSSSKSSSVHSL 1086

RESULT 11
Q9UOK6
ID Q9UOK6 PRELIMINARY; PRT: 1113 AA.
AC Q9UOK6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE BKCA ALPHA SUBUNIT.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PULMONARY ARTERY;
RA Cairns V.R., Aebly M.R., Rusch N.J.;
RT "Cloning and Characterization of BKCA Alpha Subunit from Human
RT Pulmonary Artery";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF118141; AAD31173.1; -
DR InterPro: IPR000636; -
DR InterPro: IPR002052; -
DR InterPro: IPR003066; -
DR InterPro: IPR003091; -
DR Pfam: PF00520; Ion_trans. 1.
DR PRINTS: PR00169; KCHANNEL.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_M7ASE; UNKNOWN_1.
SQ SEQUENCE 1113 AA; 125181 MW; 17A9F6259731C31 CRC64;

Query Match 41.1%; Score 2354.5; DB 4; Length 1113;
Best Local Similarity 43.4%; Pred. No. 2.2e-160;
Matches 482; Conservative 196; Mismatches 329; Indels 105; Gaps 17;

QY 26 AFILSFTFFSGILILIFRLIRSVK-KW-----QIIKGTGIIILEFTS 70
DB 24 AFLASSWVTFEGGLFIT-----LMRLTKYLMVTVCCHCGKTKKAKINNGSS-----QAD 74

QY 71 GTI-----ARSHVRLHFOGQFRDHIEMLSAQTFGVQVLYLVFLVSLIGSLIYFINS 124
DB 75 GTLKPVDKEEAAVAEYGMWTSVKDMAGVMISAOTLTGRVLYLVFLVSLIGALVIYFIDS 134

QY 125 ADPPGSSS-YEDKTIPIDLVFNAFESFYGLRPMADDKIKFLEMNSIVDITIPTE 183
DB 135 SNPIESCONFKDFTLQIDMAFNFFLLYFGLRIANDKIMFLEVNSVDFETVPVF 194

QY 184 ISYLLKSNMGLRLRLRLRLLELPQIILRAIKTSNSVSKSLSTIILSTWTFPAAGFIH 243
DB 195 VSVYLNRSWGLRLRLRLRLQFSEILQFLNLIKTSIKLVNLSIFISWTLAAGFIH 254

QY 244 LVNSGDPWLKGRNSQNSYFESIYLVWATTSTVGFDVYAKTSLGRFTIMEFTLGLSL 303
DB 255 LVNSGDPWENFQNNQALTYMECYLLMTVMTSTVGQDVYAKTTLGRLEWVFILGLIAM 314

QY 304 FANIPPEWELFANKRKYTSSEYALKGKFFLYVCGNTVDSVTFALNRLFLDKSGEINTE 363
DB 315 FASVPEIETELIGNRKKYGGSYSAVSGRKLIVYCGHTLLESVSNFLDFLKRDQDVAVE 374

QY 364 IVFLGETPPSLEETIFKCYLAATYTFISGAMKEDLRVAVESAECILIANPLCSDSH 423
DB 375 IVFLHNISPDELEALFKRHFTQVEFYOGSVLNPHDLARVKIESADACLIANKYCADPD 434


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Db 850 VNINLCDCVLLSANONNIDTSLDQKCEILASINIKSMQFDDSIGVLQANSQGETPPGM 909
QY 831 --SSDPSVSE-ETPGYNGHNEKSNCRKVPITTELKNSNIHFITQGLGESSLOET 887
Db 910 DRSSDPSVSE-ETPGYNGHNEKSNCRKVPITTELKNSNIHFITQGLGESSLOET 959
QY 888 NLHSTAFTGTVESSFFSLATAFYNYHVELLOMLTGVSSQLEQHLDKKQYGV 947
Db 960 ELYTLPFACCTAFAYSLDLSMATYFNOMLITLRTLYGATPELEALIAENALRG 1019
QY 948 ADSCSLSGNRCKGLSLSHETLSDVPRNTFGQLFCGSLDFGLICVLYRIIDE 1007
Db 1020 GYSTPOTLANDRKRVADLALDGFADLGDGCGDLFCALKTYNMLCFGIYRLDAH 1079
QY 1008 ELNPE--NKRRTVTRPANEFLPSDLVFCALPSTACRYKNEEFLQKYEIVKASOT 1065
Db 1080 LSTPQCTKRVITNPPREFELVPTDLFCMLQF-----DHNAGOSRASLSHSSHS 1130
QY 1066 TEDFRHKLSSPL 1079
Db 1131 SSSSSKSSSVHST 1144

RESULT 13
018866 PRELIMINARY; PRT: 1152 AA.
ID 018866
AC 018866:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL ALPHA SUBUNIT.
OS Sus acrota (P19).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LENS EPITHELIUM;
RA Rae J.L., Shepard A.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026000; AAB8803.1; -.
DR InterPro; IPR000636; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR002052; -.
DR InterPro; IPR003006; -.
DR Pfam; PF00520; Ion_Ctrans; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KM Ionic channel.
SQ SEQUENCE 1152 AA; 128988 MW; D62C91963D60ADBC CRC64;
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Query Match 41.1%; Score 2351.5; DB 6; Length 1152;
Best Local Similarity 43.0%; Pred. No. 3.8e-160;
Matches 485; Conservative 195; Mismatches 345; Indels 103; Gaps 17;
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Db 271 SIKLVNLLSIFSTWMLTAAGFIHLVEPSGDPWENPQNQALTYMECVYLLWMTSTVYG 330
QY 281 DYVAKTSLGRFFIMFTLGSILFANITPEVVELPANKRKTSTSEALKKFLVYCGNI 340
Db 331 DYVAKTSLGRFFIMFTLGSILFANITPEVVELPANKRKTSTSEALKKFLVYCGNI 390
QY 341 TVDSYAFRLNLDKSGEINTEIVFGETPPSLELEIFFCYLAATTFISGAMKMDL 400
Db 391 TVDSYAFRLNLDKSGEINTEIVFGETPPSLELEIFFCYLAATTFISGAMKMDL 450
QY 401 RRVAVESAEACLIANPLCSDSHADISINIRVLSIKNYDSTTRITIOILQSHMKVYLPK 460
Db 451 ARVIESADACLIANPLCSDSHADISINIRVLSIKNYDSTTRITIOILQSHMKVYLPK 510
QY 461 IPSNMWDTGNITICPAELKLFIAOGCLVPCGLFSLSPYEDONKVMKPKTKKHLINS 520
Db 511 IPSNMWDTGNITICPAELKLFIAOGCLVPCGLFSLSPYEDONKVMKPKTKKHLINS 570
QY 521 MNKILQRLSDDFAGMSFEPVAVRLCFKMYLLILAIYKSLFIDGFCGLINPPPOVRI 580
Db 571 VSNEMTEYLSAFVGLSEFVYCELFYKCLKLMAITEYKSNRBS--RIILNFGNHLKI 628
QY 581 RKNTLGFPIAETPKDVRALFYCSYCHDVFPELITNCGCKSRQHIITVSVKRMKCK 640
Db 629 QEGTLGFPIAETPKDVRALFYCSYCHDVFPELITNCGCKSRQHIITVSVKRMKCK 685
QY 641 LKGISSRISGDDSP-----PRVASTSSISNFTTRITLQHDVEDSDQLDSSGFHWCKP 694
Db 694 LKGISSRISGDDSP-----PRVASTSSISNFTTRITLQHDVEDSDQLDSSGFHWCKP 736
QY 695 TSLOKVTLRKGRKSKYKFRNHIIVACVFGDASAPKGLRNFMPLRASVYTRKELDIYFI 754
Db 736 TSLOKVTLRKGRKSKYKFRNHIIVACVFGDASAPKGLRNFMPLRASVYTRKELDIYFI 796
QY 754 GSLDYLOREMRFLRNPQIYILPGCALYSGDLHANIBQCSMCAYLSPPPQSSNQTLVD 814
Db 796 GSLDYLOREMRFLRNPQIYILPGCALYSGDLHANIBQCSMCAYLSPPPQSSNQTLVD 856
QY 815 TEALMATITISLQID-----SSDPSVSE-ETPGYNGHNEK 853
Db 853 TEALMATITISLQID-----SSDPSVSE-ETPGYNGHNEK 914
QY 854 SNCRKVPITTELKNSNIHFITQGLGESSLOETNLHSTAFTGTVESSFFSLATA 913
Db 913 SNCRKVPITTELKNSNIHFITQGLGESSLOETNLHSTAFTGTVESSFFSLATA 966
QY 914 FYNVHVELLOMLTGVSSQLEQHLDKKYGVADSCSTSLSGNRCKGLSLSHETIL 973
Db 966 FYNVHVELLOMLTGVSSQLEQHLDKKYGVADSCSTSLSGNRCKGLSLSHETIL 1026
QY 974 SDVNRNTFGQLFCGSLDFGLICVLYRIIDEELNPE--NKRRTVTRPANEFLPSD 1031
Db 1026 SDVNRNTFGQLFCGSLDFGLICVLYRIIDEELNPE--NKRRTVTRPANEFLPSD 1086
QY 1032 LVFCAIPSTACRYKNEEFLQKYEIVNKASQTTEDFRHKLSSPL 1079
Db 1086 LVFCAIPSTACRYKNEEFLQKYEIVNKASQTTEDFRHKLSSPL 1125

RESULT 14
008460 PRELIMINARY; PRT: 1196 AA.
ID 008460
AC 008460: 064703;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE SLOWPOKE HOMOLOG. POTASSIUM CHANNEL. CALCIUM-ACTIVATED (CALCIUM-
DE ACTIVATED POTASSIUM CHANNEL) (SLOWPOKE HOMOLOG PROTEIN).
GN KCMAL OR SLO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
```


KW Ionic channel.
SQ SEQUENCE 1118 AA: 125843 MW: 535DA3DBAE87A47 CRC64:

Query Match 41.18; Score 2349.5; DB 13; Length 1118;
Best Local Similarity 44.08; Pred. No. 5.1e-160;
Matches 487; Conservative 183; Mismatches 349; Indels 89; Gaps 16;

OY 26 AFIISSFFVTFSGLIILILIFRLIRSVK-KW-----QIIIGTGIIIELETFSG 71
DB 24 AFLASSNVTFFGGLEFIT---LIMRTLYLMTVVCCHCGVKKKEAKIKGGG---DTQADG 76
OY 72 TIARSHVR-----SLHFQGFQRDHIEMLLSAQTFVGQVLYLVFVLSIGSLIYFINS 125
DB 77 ACKPTDEKEENVAAVEGVTSMWAGVIMISAQTLTGVLVLFVLSIGALVITFISS 136
OY 126 DPGVSCSS-YEDKTIPIIDLVNAPFSPFGURFMAADKIKFMLEMNSIVDIFIIPTPTI 184
DB 137 NPISCONFYKDFDLOIDMAFNVEFLLYFGRLTAANDKLMFMLEVNSVVDFTVPVFEV 196
OY 185 SYLKSNNLGLRFLRALRLLELPOLITLRAIKTNSVYKFSKLSLIISTWTAGFTHL 244
DB 197 SVYLRNRSWLGRLRALRLIOFSEILOFLNLTKTSNLIKLVNLCSTFTWLTAGFTHL 256
OY 245 VENGSDPMLKGRNSQNSISYFESIYLVNATSTVGEGDVAAKTSIGRTPEIMEFTIGSLIF 304
DB 257 VENGSDPMPENQNNQOOLYWECCVLLAMWTMGVGDYAKTTLGRLFMVFILGGLAMF 316
OY 305 ANYIPENVELFANKRKRTYSSYEALKGKKEFYVCGNITVDSVTAFLRNLFRDKSGEINTEI 364
DB 317 ASYVPEIIEILGNRRKKYGGYSAVSGRKHIVCGHITLESYNFLKDFLHRKDRDQVNEI 376
OY 365 VFLGETPSELEIEIFKCYLATTFTFISGAMKWEDELRYVAESAECILIANPLCSDSHA 424
DB 377 VFLNINISNLELEALFKHFTQVEYQSVLPNHDLARVIESADACILIANKICADPDA 436
OY 425 EDISINIMKVLISIKNVDSYTRIIIOLOSNNKVVYLPKIPSNMMDGDNIIICFAELKGFIA 484
DB 437 EDASINIMKVISIKNVHPIRITITQMLQYNNKAHLNIPSNMKEGDDAICLAELKGFIA 496
OY 485 QGCLVPGICLFTFLSLFEQNNKKNPKOTKKHFLNSMKNNKILTORLSDDFAGMSPEVAR 544
DB 497 QSCILAPGISTMLANLFMSRSFIKIIEEDTWQKYLEGVANEMYETELSSAFVGLSEPAVCE 556
OY 545 LCFIKMYLLAIIEYKSLFTDGFCC--GLINPPQVIRIKNTLGFETAPKDVRAFLFY 602
DB 557 LVFAKLKMLLAIEIKSEKRSRKRRLILNPGNHVKIQEGTGLFFLASDAKEVARAFY 616
OY 603 CSVCHDVFIFELITNCGCKSRSRQHTVPSVKRMKCKLKGISRSISGQDSP-----PR 656
DB 617 CKACHDDITDPKRIKKCGCK---RLEDQPTSLSPKKKQNGMGMRNSPNSPKLMRHDP 673
OY 657 VSASTSSISNFTTTLQHDVEQDSQDLSGGMFHCKPTSLDKVTLKRKGSKYKFRNHI 716
DB 674 LIPNEQIDN-----MDANVKKYDSTGMFWCSPAKDIEKVIILTRSEAMFVLSGHV 724
OY 717 VACVGDASHAPMGLRNFVPLRASNYRKEIKDQIVFISLDYLOREWRFLRNPOIYIL 776
DB 725 VVCIFGDKYKSLIGRLNLYMPLRASNFHYHEKRLIVFSGLEYLKREMETLHNPKVLSIL 784
OY 777 PGCALYSGDLHAANIEOCSMCVAVLPPQPSNQTLVDTEAIMATLTIGSLQID----- 830
DB 785 PGFTPLSRADLRAVININLCDMCVILSANQNNIDDAISLQKECIASLNKISQFDOSIGVL 844
OY 831 -----SSSPSPSPSVS-EETPGYTNHNEKSNCRKVPILTELKNPSPNHFIE 875
DB 845 QANSQGFPPGMDSRSPDSSPVHGLLRQPSITTGAN-----IPITELVNDSSNVQFLD 897
OY 876 QUGGLESLQETNLHLSTAFNGTVFSSFLDSLATAFYNYHYELLOMLTVGGVSSOL 935
DB 898 Q-----DDDDPPTLEKLTQPFACGTAFVAVSDLSMSATYFENDNIIITLITLVGTGAPEL 954
OY 936 EOHLDKDKVYGVADSCSTLSLGRNRCGLGLSLHETILSDVNPRTFQGLFCGSLDLFGI 995

DB 955 EALLAEENALRGYSTPOTLANRRRCRVAAQLALVDGPFADLGDCGYGDLFCALKATYNM 1014
OY 996 LCVGLYRIIDEEELNPE--NKRFTYTRANEFKLLPSDLYVCALPF-----STACYK 1045
DB 1015 LCFGIYRLDAHLSTPSQCTRRYVITNPEYFELVPTDLIFCLQFDHMGOSRASLSHS 1074
OY 1046 RNEEFSLOKSYEIVNKKASQTEDETFRRHK 1073
DB 1075 SHSSYSSKSSSVHSTPSTANRRRTK 1102

Search completed: October 5, 2001, 12:14:27
Job time: 629 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 5, 2001, 12:12:21 ; Search time 29.2 Seconds

(without alignments)
1296.312 Million cell updates/sec

Title: US-09-176-664-16

Perfect score: 5722
Sequence: 1 MFQTKLRNETMEDLPKMSCT.....CIHQSLTSLRELTPLSLK 1105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	216.5	3.8	209 1 Y139_METJA	Q57603 methanococ
2	162	2.8	806 1 CIRB_CANFA	Q95167 canis fam1
3	158.5	2.8	853 1 CIRK_RAT	P15387 rattus norv
4	158.5	2.8	854 1 CIRK_HUMAN	Q14721 homo sapien
5	158	2.8	802 1 CIRB_RAT	Q63099 rattus norv
6	157	2.7	924 1 CIRK_DROME	P17970 drosophila
7	154.5	2.7	806 1 CIRB_HUMAN	Q92953 homo sapien
8	147	2.6	499 1 CIRK_HUMAN	P15389 homo sapien
9	144	2.5	499 1 CIRK_MOUSE	P15386 mus musculu
10	143.5	2.5	499 1 CIRK_XENLA	P22739 xenopus lae
11	143.5	2.5	433 1 YD57_METJA	Q58752 methanococ
12	143.5	2.5	676 1 CIRI_HUMAN	P51787 homo sapien
13	140	2.4	604 1 CIRI_MOUSE	P97414 mus musculu
14	139.5	2.4	643 1 CIRK_DROME	P08511 drosophila
15	139.5	2.4	656 1 CIRK_DROME	P08513 drosophila
16	139	2.4	691 1 TOKI_YEAST	P40310 saccharomyc
17	138.5	2.4	616 1 CIRI_DROME	P08510 drosophila
18	136	2.4	757 1 CIRK_HUMAN	Q14003 homo sapien
19	135.5	2.4	490 1 CIRK_DROME	P17971 drosophila
20	135	2.4	889 1 CIRK_RAT	Q01956 rattus norv
21	133	2.3	769 1 CIRK_MOUSE	Q06199 mus musculu
22	132.5	2.3	1174 1 CIRK_DROME	Q02280 drosophila
23	131.5	2.3	498 1 CIRK_DROME	P17972 drosophila
24	131.5	2.3	1032 1 MT18_YEAST	P40469 saccharomyc
25	131	2.3	638 1 CIRK_RAT	P27462 rattus norv
26	131	2.3	872 1 CIRI_HUMAN	Q43525 homo sapien
27	129.5	2.3	2164 1 POLG_HRB9	P07210 human rhino
28	129	2.3	1581 1 ARO1_PNECA	P01659 p pentafunc
29	125.5	2.2	518 1 CIRK_MOUSE	P16390 mus musculu
30	123	2.1	417 1 KCH_ECOLI	P31069 escherichia
31	122.5	2.1	523 1 CIRK_HUMAN	P22001 homo sapien
32	122.5	2.1	525 1 CIRK_RAT	P15384 rattus norv
33	121	2.1	530 1 CIRK_RAT	P17659 rattus norv

34	120.5	2.1	511 1 CIRK_HUMAN	P48547 homo sapien
35	120.5	2.1	511 1 CIRK_MOUSE	P15388 mus musculu
36	120.5	2.1	585 1 CIRK_RAT	P25122 rattus norv
37	120.5	2.1	1001 1 CIRK_DROME	Q94526 drosophila
38	120	2.1	2171 1 CIRK_RAT	P15381 oryctolagus
39	118.5	2.1	902 1 POLG_PVYN	Q14053 schizosacch
40	118.5	2.1	3063 1 POLG_PVYN	P18247 p genome po
41	117.5	2.1	541 1 NUSM_ARTSF	Q37710 artemisa san
42	117	2.0	495 1 CIRI_HUMAN	Q09470 homo sapien
43	117	2.0	695 1 CIRI_HUMAN	P56596 homo sapien
44	116.5	2.0	495 1 CIRI_MOUSE	P16388 mus musculu
45	116.5	2.0	495 1 CIRI_RAT	P10499 rattus norv

ALIGNMENTS

```

RESULT 1
ID Y139_METJA STANDARD: PRT; 209 AA.
AC Q57603:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0139.
GN MJ0139.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback L.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii."
RT Science 273:1058-1073(1996).
RL -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: SOME TO POTASSIUM CHANNEL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U67471; AAB98122.1; -.
DR TIGR: MJ0139; -.
DR InterPro: IPR000636; -.
DR Pfam: PF00520; Ion_Trans; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 11
FT TRANSMEM 72
FT TRANSMEM 126
FT TRANSMEM 157
FT TRANSMEM 177
FT TRANSMEM 182
FT TRANSMEM 202
SQ SEQUENCE 209 AA; 24183 MW; FC91E7320F34D90F CRC64;

```

Query Match 3.8%; Score 216.5; DB 1; Length 209;
Best Local Similarity 25.9%; Pred. No. 1.4e-07;
Matches 60; Conservative 55; Mismatches 80; Indels 37; Gaps 7;

```

OY 103 QVLTIVLVLSIGSLTIFINSADPSCSSYEDKTPIDVLVFNFSFGLRPMADD 162
OY 104 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 KIMEVLSLFFFEIYVASTLTSTYN-----PYQDLITLIDYISINEFFFEIYNYVED 64
OY 163 KIKFWLEMSNIIVDTFTPTPTISYLLK---SNMGLRFLRALRLLEDPQILQILRAIKT 218
OY 164 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 KAKFFKFDIYNIVDAIV--IAFLVSLAGVFSKAFGLRVINILRLIVLRIKRLKEEN 123
OY 219 SNAVKFSKLSLITLSTWTAAGFIHLVENSDDPKLKGNSONISFEESILYMATTSYVG 278
OY 220 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 QALNFLTLLTIC---FIASCLMIYVSSGNPAIN-----NFDAPFYFTTISITVVG 172
OY 279 FGDVAKTSLGRFTMFTPLGSLIFANVIEPMELFANKRKYSYSYALNG 330
OY 280 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 YGDITPKTDACKLIIIF-----SVLEFFISGL-----ITSLOKALNG 208

RESULT 2
CIRB_CANFA ID CIRB_CANFA STANDARD; PRT; 806 AA.
AC Q95167;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.2.
GN KCNB2.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrate; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID:9615;
RN R1
RP SEQUENCE FROM N.A.
RX MEDLINE-98275219; Pubmed-9612272;
RA Schmalz F., Kinsella J., Koh S.D., Vogalis F., Schneider A.,
RA Flynn E.R., Kenyon J.L., Horowitz B.;
RT "Molecular identification of a component of delayed rectifier current
RT in gastrointestinal smooth muscles."
RT Am. J. Physiol. 274:G901-G911(1998).
CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -!- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -!- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
CC
CC EMBL; U69963; AB08432.1; -.
CC DR InterPro: IPR000636; -.
CC DR InterPro: IPR003091; -.
CC DR Pfam: PF00520; Ion.trans. 1.
CC DR PRINTS: PRO0169; KCHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation.
CC FT DOMAIN 1 190 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 191 212 SEGMENT S1 (POTENTIAL).
CC FT DOMAIN 213 232 EXTRACELLULAR (POTENTIAL).
CC FT TRANSSEM 233 254 SEGMENT S2 (POTENTIAL).

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FT	DOMAIN	255	264	CYTOPLASMIC (POTENTIAL)
FT	TRANSEM	265	286	SEGMENT S3 (POTENTIAL)
FT	DOMAIN	287	298	EXTRACELLULAR (POTENTIAL)
FT	TRANSEM	299	320	SEGMENT S4 (POTENTIAL)
FT	DOMAIN	321	334	CYTOPLASMIC (POTENTIAL)
FT	TRANSEM	335	356	SEGMENT S5 (POTENTIAL)
FT	DOMAIN	357	396	EXTRACELLULAR (POTENTIAL)
FT	TRANSEM	397	418	SEGMENT S6 (POTENTIAL)
FT	DOMAIN	419	806	CYTOPLASMIC (POTENTIAL)
FT	CARBOHYD	287	287	N-LINKED (GLCNAC. . .) (POTENTIAL)
SO	SEQUENCE	806 AA;	90283 MW;	D962EC256760B743 CRC64;

Query Match	2.88;	Score 162;	DB 1;	Length 806;
Best Local Similarity	22.88;	Pred. No. 0.0041;		
Matches 63;	Conservative	62;	Mismatches 109;	Indels 42;
				Gaps 8;

QY	88	RDHTEMLLSAQTFPGOVVILVFLVSLGSLIFETNSADPVGSCSSY-----EDKTIPID	142
Db	180	RDLEKPRNS--SVAKILAIYSNLFYISTALSLINTLPELOEMDEFOCPDNDQOLAVE	237
QY	143	LVNFAFSEFYEGFLRPMADDKIKFWLENNISVIDIFTPTPTISYLL-KSNMLGLRFLRAL	201
Db	238	AVCNAMFTMEYLLRFLSPNKKWKEFGPLNYDLALIPYVTFITPTESKNSVLOFQVNR	297
QY	202	RLLELPQLOLLRLAKIKTSNSV-----KFSKLSLITLSWTFPAAC-----FIH	243
Db	298	RVOYIFRIMRLIRLIKLRHSTGLQSLGFTLRNSYNELGLIL--FLAMGIMFSSLVF	354
QY	244	LVENSGDFMLGRNSQNSYFESIYLVWATSTVGFQGVNAKTSIGRFIFFTGLSLIL	303
Db	355	FAEKDADA-----TKFISIPASFWMATITMTYVGYGIYKTLIGKSVGLGCIAGLV	408
QY	304	PANTPEKVELFA-----NKKRYTSEYELKCKK	332
Db	409	IALPIPIIVPFSEFYKQKROEKAIKRREALLERAK	444

RESULT	3
CIRKA_RAT	STANDARD; PRT; 853 AA.
ID	CIRKA_RAT.
AC	P15387;
DT	01-APR-1990 (Rel. 14, Created)
DT	01-AUG-1990 (Rel. 15, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).
GN	KCNB1.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=89365157; PubMed=2770868.
RA	Frech G.C., Vandongen A.M.J., Schuster G., Brown A.M., Joho R.H.;
RT	"A novel potassium channel with delayed rectifier properties isolated
RT	from rat brain by expression cloning.";
RL	Nature 340:642-645(1989).
RN	[2]
RP	REVISIONS.
RA	Frech G.C.;
RL	Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC	POTENTIAL.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-1- TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS IN
CC	THE CEREBRAL CORTEX, FOLLOWED BY THE HIPPOCAMPUS, CEREBELLUM, AND
CC	OLFACATORY BULB. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN

CC RETINA AND KIDNEY. ALSO PRESENT IN CARDIAC MUSCLE TISSUE OF THE
CC ATRIUM AND VENTRICLE AND IN SKELETAL MUSCLE.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X16476; CAA34497.1; -
CC PIR: S05448; CHRTD1.
CC InterPro: IPR000636; -
CC InterPro: IPR003091; -
CC Pfam: PF00520; Ion_trans; 1.
CC PRINTS: PR00169; KCHANNEL.
CC KW Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
CC Ionic channel; Multigene family; Phosphorylation.
CC FT DOMAIN 1 182
FT TRANSMEM 183 204
FT TRANSMEM 205 224
FT TRANSMEM 225 246
FT TRANSMEM 247 256
FT TRANSMEM 257 278
FT TRANSMEM 279 290
FT TRANSMEM 291 312
FT DOMAIN 313 326
FT TRANSMEM 327 348
FT TRANSMEM 349 388
FT TRANSMEM 389 410
FT DOMAIN 411 853
FT CARBOHYD 279 279
FT MOD_RES 440 440
FT MOD_RES 492 492
FT MOD_RES 95280 MM; 7A08998839716165 CRC64;
FT SEQUENCE 853 AA; 95280 MM; 7A08998839716165 CRC64;
SO

Query Match 2.8%; Score 158.5; DB 1; Length 853;
Best Local Similarity 22.6%; Pred. No. 0.0075;
Matches 65; Conservative 64; Mismatches 123; Indels 35; Gaps 8;

OY 103 QVVLVIVVLSGLIIFINSADVSGSSIEDT-----IPDLVFAFSPFGRLF 157
DB 185 KILALISIMFYLSIALSLNLPQLQSDERGSTDNPOLAHVAVCAMFTMEYLA 244
OY 158 MAADKIKFMLEMNSIVDFITPFIISYVL-KSNMGLRRLARLEPOLIOLRAI 216
DB 245 LSSPKKMFEPKPLAIDLALPLFYVIFLTESKSVYQFONRVVOIFIMKRLRL 304
OY 217 KTSNSVKFSKLSLILSTWETAAGFIHLVENSQDPLK-----GRNSONISYEESI- 267
DB 305 KLARSTGLQSLGFTLRSYNELGLLFLWGMIFSSLVFAEKDEDDTKFSIPASF 364
OY 268 YLVAMTITVGCGDVVATSLGRTIMFTYLSLLFANVTIEMELPA-----NKRK 320
DB 365 WVAITMTVTGGDILPTLGLKIVGLCCAGVLAIVLPIIYNNSEFYKEOKROK 424
OY 321 YTSYEALKGKFIYVCGN---ITVSYTAFLR-----NFLRDKSGE 359
DB 425 AKRREALERAK-----RNGSIVSNMMDAFARSIEMMDIYERKKE 466

RESULT 4
ID CIRA_HUMAN STANDARD: PRT: 854 AA.
AC Q14721;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DHK1).
GN KCB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda S.R., Soler F., Zuhke R.D., Joho R.H., Lewis D.L.;
RL Submitted (JAN-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSURING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
CC EMBL: L02840; AAA36156.1; -
CC MIM: 600397; -
CC InterPro: IPR000636; -
CC InterPro: IPR003091; -
CC Pfam: PF00520; Ion_trans; 1.
CC PRINTS: PR00169; KCHANNEL.
CC KW Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
CC Ionic channel; Multigene family; Phosphorylation.
CC FT DOMAIN 1 182
FT TRANSMEM 183 204
FT TRANSMEM 205 224
FT TRANSMEM 225 246
FT TRANSMEM 247 256
FT TRANSMEM 257 278
FT TRANSMEM 279 290
FT TRANSMEM 291 312
FT TRANSMEM 313 326
FT TRANSMEM 327 348
FT TRANSMEM 349 388
FT TRANSMEM 389 410
FT DOMAIN 411 854
FT MOD_RES 440 440
FT MOD_RES 492 492
FT MOD_RES 95521 MM; 360DEB3E45731EDA CRC64;
FT CARBOHYD 279 279
FT SEQUENCE 854 AA; 95521 MM; 360DEB3E45731EDA CRC64;
SO

Query Match 2.8%; Score 158.5; DB 1; Length 854;
Best Local Similarity 22.6%; Pred. No. 0.0075;
Matches 65; Conservative 64; Mismatches 123; Indels 35; Gaps 8;

OY 103 QVLIIVFVLSIGSLIYFINSADPVGSCSYEDKT-----IPDLVFNAFESFYEGLR 157
 DB 185 KILAIISIMFVLSLSTALSLNTLPELOSLDEFSGSTDPNOLAHVEAVCIAMFTMEYLRF 244
 OY 158 MAADKIKFMLEMNSIYDIFIPPTFISYLL-KSNMGLRFLRALRLLEPQIOLILRAI 216
 DB 245 LSSKKKKFRRGPLNADLAILDPIYVYIFLTSNKSVMLOFQNVRRVVOIFRIMRLKIL 304
 OY 217 KTSNSVFSKLSLSTLSTWFTAGFIHLVENSQDPWLK-----GRNSQINISYFESI--- 267
 DB 305 KLANHSTGLQSLGFTLRNSVNEGLLLFLAMGIMISLVFFAEKDEDDTKFKSIFASF 364
 OY 268 YLVWATTSYVGFQDVYAKTSLGRTFIMFTLGLILFANYPVEVELFA-----NKRK 320
 DB 365 WMATITMTVTGYGDIYDKPILTKIYVGLCCAGVIALPIPIIVNFSSEFYKQKROEK 424
 OY 321 YTSYSEALCKKRFIVCGN---ITVDSVTAFLR-----NFLRDSKE 359
 DB 425 AIKRRERLERAK-----RNGSIYSNMKDAFARSIEMMDIYVERNGE 466

RESULT 5

CIRB_RAT STANDARD; PRT; 802 AA.

AC 063099;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.2 (CDRK).
 GN KCBM2.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
 RX MDLINE=92198655; PubMed=1550672;

RA Huang P.M., Glatz C.E., Bret D.S., Yellen G., Snyder S.H.;

RT A novel K⁺ channel with unique localizations in mammalian brain:
 RT molecular cloning and characterization.";

RU Neuron 8:473-481(1992).
 CC -|- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.

CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -|- TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS IN
 CC THE OLFACTORY BULB, FOLLOWED BY THE CEREBRAL CORTEX, HIPPOCAMPUS,
 CC AND CEREBELLUM. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN
 CC WHOLE TONGUE EPITHELIUM AND CIRCUMVALLATE PAPILLAE.

CC -|- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.

CC -|- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.

CC -|- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.

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CC EMBL: M77482; AAA40905.1; -
 CC DR InterPro: IPR000636; -.

DR InterPro: IPR003091; -
 DR Pfam: PF00520; Ion_trans. 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT DOMAIN 1 190
 FT TRANSMEM 191 212
 FT DOMAIN 213 232
 FT TRANSMEM 233 254
 FT DOMAIN 255 264
 FT TRANSMEM 265 286
 FT DOMAIN 287 298
 FT TRANSMEM 299 320
 FT DOMAIN 321 334
 FT TRANSMEM 335 356
 FT DOMAIN 357 396
 FT TRANSMEM 397 418
 FT DOMAIN 419 802
 FT DOMAIN 528 531
 FT CARBOHYD 287 287
 FT SEQUENCE 802 AA; 90702 MW; 792CC09A5DB28D7F CRC64;

Query Match 2.8%; Score 158; DB 1; Length 802;
 Best Local Similarity 23.7%; Pred. No. 0.0074;
 Matches 60; Conservative 55; Mismatches 114; Indels 24; Gaps 6;

OY 103 QVLIIVFVLSIGSLIYFINSADPVGSCSYEDKTIPDLVFNAFESFYEGLR 156
 DB 193 KILAIIVSLFVLSLSTALSLNTLPELOENDEFGQPSD-NKRKLAHVEAVCIAMFTMEYLRL 251
 OY 157 FMAADKIKFMLEMNSIYDIFIPPTFISYLL-KSNMGLRFLRALRLLEPQIOLILRAI 215
 DB 252 FLSSPMKFKFRGPLNADLAILDPIYVYIFLTSNKSVMLOFQNVRRVVOIFRIMRLKIL 311
 OY 216 KTSNSVFSKLSLSTLSTWFTAGFIHLVENSQDPWLK-----GRNSQINISYFESI--- 267
 DB 312 KLANHSTGLQSLGFTLRNSVNEGLLLFLAMGIMISLVFFAEKDEDDTKFKSIFASF 371
 OY 268 YLVWATTSYVGFQDVYAKTSLGRTFIMFTLGLILFANYPVEVELFA-----NKRK 319
 DB 372 FWMATITMTVTGYGDIYDKPILTKIYVGLCCAGVIALPIPIIVNFSSEFYKQKROEK 431
 OY 320 KYTSSYSEALCKKRFIVCGN---ITVDSVTAFLR-----NFLRDSKE 352
 DB 432 KAIRRERLERAK 444

RESULT 6

CIRB_DROME STANDARD; PRT; 924 AA.

AC P17970;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAB (SHAB1).
 GN SHAB OR SHAB1.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Ephydroidea; Mecoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OX NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MDLINE=90239553; PubMed=2333511;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;

RT "K⁺ current diversity is produced by an extended gene family
 conserved in Drosophila and mouse.";
 RL Science. 248:599-603(1990).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MDLINE=90245658; PubMed=2336395;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;


```

"Shal", Shab, and Shaw: three genes encoding potassium channels in
Drosophila."
RL Nucleic Acids Res. 18:2173-2174(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROOTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
-----
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DR EMBL; M32659; AAA28896.1; -.
DR PIR; S15058; S15058.
DR HSSP; P01551; IACX.
DR FLYBase; FBgn000383; Shab.
DR InterPro; IPR000636; -.
DR InterPro; IPR003091; -.
DR Pfam; PF00520; Ion_Trans; 1.
DR PRINTS; PR00169; KCHANNEL.
DR KMW Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
RV Ionic channel; Transmembrane; Phosphorylation.
FT TRANSMEM 436 454 SEGMENT S1.
FT TRANSMEM 474 495 SEGMENT S2.
FT TRANSMEM 506 527 SEGMENT S3.
FT TRANSMEM 536 561 SEGMENT S4.
FT TRANSMEM 577 598 SEGMENT S5.
FT TRANSMEM 638 659 SEGMENT S6.
FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 749 749 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 756 756 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 885 885 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 888 888 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 690 690 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 731 731 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 796 796 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
SQ SEQUENCE 924 AA; 99698 MM; FAF74205C7020758 CRC64;

Query Match 2.7%; Score 157; DB 1; Length 924;
Best Local Similarity 23.1%; Pred. No. 0.011;
Matches 75; Conservative 69; Mismatches 125; Indels 56; Gaps 11;

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OY 235 MFTAGFIHVENSGDPWLKGRNSQNSIFESIYLVMTSTVGRGVVAKTSLGRFTIM 294
DB 591 FSSLLATVEKDE-----KDTKFSVPEAFWAGITVTGVDIGPTALGKVIQT 641
OY 295 PFTGLSLIFANYPIDEWELPA-----NKRKYSSYEALGKKFIYVCGNITVDSTYA 347
DB 642 VCCICGVLVLPPIITVINNFAPFKNMREKALKRREALDRAK-----RGSLIVS 693
OY 348 FLRNFLRD---KSGEINTEIYFLGE 369
DB 694 FHHMLKDAFAKSMOLIDIVDTGK 718

RESULT 7
CIRB_HUMAN STANDARD; PRT; 806 AA.
AC 092953;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.2.
GN KCNB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98275219; Pubmed=9612272;
RA Schmalz F., Kinsella J., Koh S.D., Vogalis F., Schneider A.,
RA Flynn E.R., Kenyon J.L., Horowitz B.;
RT "Molecular identification of a component of delayed rectifier current
RT in gastrointestinal smooth muscles."
RL Am. J. Physiol. 274:G901-G911(1998).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
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-----
DR EMBL; U69962; AAB08433.1; -.
DR InterPro; IPR000636; -.
DR InterPro; IPR003091; -.
DR Pfam; PF00520; Ion_Trans; 1.
DR PRINTS; PR00169; KCHANNEL.
RV Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 191 190 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 213 212 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 233 232 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 255 254 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 265 264 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 287 298 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 287 298

```


OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090, 10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat;
 RX MEDLINE=89255260; PubMed=2722779;
 RA McKinnon D.;
 RT "Isolation of a cDNA clone coding for a putative second potassium
 channel indicates the existence of a gene family.";
 RT J. Biol. Chem. 264:8230-8236(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat; TISSUE=Brain;
 RX MEDLINE=90059914; PubMed=2555158;
 RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 Stocker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 channels in mammalian brain.";
 RT EMBO J. 8:3235-3244(1989).
 RN [3]
 RP REVISIONS;
 RA Ludwig J.;
 RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat;
 RX MEDLINE=91352097; PubMed=1715584;
 RA Paulmichl M., Nasimith P., Herlitz R., Reed K., Boyle W.A.,
 RA Nedoume J.M., Peralta E.G., Clapham D.E.;
 RT "Cloning and expression of a rat cardiac delayed rectifier potassium
 channel.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:7892-7895(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Mouse;
 RX MEDLINE=90161996; PubMed=2305265;
 RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
 RA Ghanshani S., Tempel B.L., Gutman G.A.;
 RT "A family of three mouse potassium channel genes with intronless
 RT coding regions.";
 RT Science 247:973-975(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL: J04731; AAA40819.1; -;
 DR EMBL: X16003; CAA34134.1; -;
 DR EMBL: M74449; AAA19867.1; -;
 DR EMBL: M30440; AAA39713.1; -;
 DR PIR: A33814; A33814.
 DR PIR: S06709; S06709.

DR PIR: B40090; B40090.
 DR HSP: P03621; 21FN.
 DR MGD: MG1:96659; Kcna2.
 DR InterPro: IPR000636; -.
 DR InterPro: IPR003091; -.
 DR Pfam: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane.
 KW Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
 FT TRANSMEM 164 182
 FT TRANSMEM 222 243
 FT TRANSMEM 222 243
 FT TRANSMEM 255 275
 FT TRANSMEM 293 311
 FT TRANSMEM 328 347
 FT TRANSMEM 389 411
 FT CARBOHYD 38 38
 FT CARBOHYD 207 207
 FT MOD_RES 449 449
 FT CONFLICT 411 411
 FT SEQUENCE 499 AA; 56700 MM; ABFEA6F3F59AF42A CRC64;
 SO
 Query Match 2.5%; Score 144; DB 1; Length 499;
 Best Local Similarity 22.0%; Pred. No. 0.032;
 Matches 76; Conservative 65; Mismatches 132; Indels 72; Gaps 13;
 QY 104 VLVLVLEVLST-----GSLITVINSADPVG--SCSYDEKTPIDLVF 145
 DB 170 VMVLISVLSCTLEPLFRDENDMHGGVTFHTYSSTIGYQOSTFSDPPFIVERLC 229
 QY 146 NAFSEYFGLRFMAADDKIKFMLEMNSIVDFTIPPFISYLR-----SNMIG 194
 DB 230 IIMSEFVLVFFACPSKAGFTNIMIDVAILPFIITGLTSLAEKPEDAOCQOAMS 289
 QY 195 LRTLRALRLLELPQI-----LQIL-RAIKTS---NSVKFSKLISILSTWTAAG 240
 DB 290 LAIRLVILVAVFRIKLSRHSKSLQILGQTLKASMRGLILFPLFGVIL--FSSAV 346
 QY 241 FHLVENSQDWLGRNSQNSYFESIYLVMASTYQFGGVAKTSLGRFIMFPLGS 300
 DB 347 YFAEDE-----RDSQFSPIDAEFWAVSMVGYGMVPTTIGGKIVGSLCALAG 398
 QY 301 LILFANTYPEWVELFANKRYTSSVEALKGKFTIV--CGNI-----TVDSVTAFLR 350
 DB 399 VLTALPVPVIVSNF--NYFHRTEGEQAOYIQVTSCTPIPSPLDKRSASTISKS 456
 QY 351 NFLDKSGEINTEIVFGLGTPPSLEETIFKCYLAITTFISGSAM 395
 DB 457 DYMEIQEGVNSNDFREE-----NLKTA-NCTILANTVYVITKM 495
 RESULT 10
 CIRK2_XENLA
 ID CIRK2_XENLA STANDARD; PRT; 499 AA.
 AC P22739;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.2 (XSHA2).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 CC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91026051; PubMed=2223094;
 RA Ribera A.B.;
 RT "A potassium channel gene is expressed at neural induction.";
 RT Neuron 5:691-701(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

Db 258 DEVEDIELRKFKVIEKDESLAY--KSLKDNIRKGTATIGIRREKFCINPYPE 311

RESULT 12

C101_HUMAN STANDARD; PRT; 676 AA.

ID C101_HUMAN

AC P51787; Q92960; O00347; O60607;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, last sequence update)

DT 01-OCT-2000 (Rel. 40, last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE 1 (KVL 9).

GN KCNQ1 OR KCNA9 OR KVLQ1 OR KCNA8.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=97459933; PubMed=9312006;

RA Chouabe C., Neyroud N., Guicheney P., Lazdunski M., Romey G.,

RT "Properties of KVLQ1 K+ channel mutations in Romano-Ward and Jervell

RT and Lange-Nielsen inherited cardiac arrhythmias.";

RL EMO J. 16:5472-5479(1997).

RN [2]

RP SEQUENCE OF 96-156 FROM N.A.

RC TISSUE=Pancreas;

RX MEDLINE=9705936; PubMed=8900283;

RA Sanguinetti M.C., Curran M.E., Zou A., Shen J., Spector P.S.,

RT "Coassembly of K(V)Q1 and minK (Isk) proteins to form cardiac I(Ks)

RT potassium channel.";

RL Nature 384:80-83(1996).

RN [3]

RP SEQUENCE OF 1-129 FROM N.A.

RX MEDLINE=97268689; PubMed=9108097;

RA Yang W.P., Levesque P.C., Little W.A., Conder M.L., Shalaby F.Y.,

RA Blamir M.A.;

RT "KVLQ1, a voltage-gated potassium channel responsible for human

RT cardiac arrhythmias.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:4017-4021(1997).

RN [4]

RP SEQUENCE OF 130-676 FROM N.A., AND VARIANTS LQ1.

RX MEDLINE=96122034; PubMed=8528244;

RA Wang Q., Curran M.E., Splawski I., Burn T.C., Millholland J.M.,

RA Varrault T.J., Shen J., Timothy K.W., Vincent G.M., de Jager T.,

RA Schwartz P.J., Towbin J.A., Moss A.J., Atkinson D.L., Landes G.M.,

RA Connors T.D., Keating M.T.;

RT "Positional cloning of a novel potassium channel gene: KVLQ1

RT mutations cause cardiac arrhythmias.";

RL Nat. Genet. 12:17-23(1996).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM TKVLO1).

RC TISSUE=Heart;

RX MEDLINE=97450920; PubMed=9305853;

RA Jiang M., Tseng-Crank J., Tseng G.-N.;

RT "Suppression of slow delayed rectifier current by a truncated isoform

RT of KVLQ1 cloned from normal human heart.";

RL J. Biol. Chem. 272:24109-24112(1997).

RN [6]

RP VARIANTS LQ1 SER-314 AND VAL-341.

RX MEDLINE=97026293; PubMed=8872472;

RA Russell M.W., Dick M. II, Collins F.S., Brody L.C.;

RT "KVLQ1 mutations in three families with familial or sporadic long QT

RT syndrome.";

RL Hum. Mol. Genet. 5:1319-1324(1996).

RN [7]

RP VARIANTS LQ1 PRO-178; MET-313; ARG-325 AND PRO-366.

RX MEDLINE=97176600; PubMed=9024139;

RA Tanaka T., Nagai R., Tomotake H., Takata S., Yano K., Yabuta K.,

RA Haneda N., Nakano O., Shibata A., Sawayama T., Kasai H., Yazaki Y.,

RA Nakamura Y.;

RT "Four novel KVLQ1 and four novel HERG mutations in familial long-QT

RT syndrome.";

RL Circulation 95:565-567(1997).

RN [8]

RP VARIANTS LQ1.

RX MEDLINE=98045903; PubMed=9386136;

RA Donger C., Denjoy I., Berthet M., Neyroud N., Cruaud C., Benaecour M.,

RA Chivoret G., Schwartz K., Coumel P., Guicheney P.;

RT "KVLQ1 C-terminal missense mutation causes a forme fruste long-QT

RT syndrome.";

RL Circulation 96:2778-2781(1997).

RN [9]

RP VARIANT LQ1 ARG-216.

RX MEDLINE=97418118; PubMed=9272155;

RA van den Berg M.H., Wilde A.A.M., Rodles de Medina E.O., Meyer H.,

RA Geelen J.L.M.C., Jongbloed R.J.E., Wellens H.J., Geraedts J.P.M.;

RT "The long QT syndrome: a novel missense mutation in the S6 region of

RT the KVLQ1 gene.";

RL Hum. Genet. 100:356-361(1997).

RN [10]

RP VARIANT LQ1 ASN-317.

RX MEDLINE=98027069; PubMed=9302275;

RA Wolinik B., Schroeder B.C., Kubisch C., Esperer H.D., Wleack P.,

RA Jentsch T.J.;

RT "Pathophysiological mechanisms of dominant and recessive KVLQ1 K+

RT channel mutations found in inherited cardiac arrhythmias.";

RL Hum. Mol. Genet. 6:1943-1949(1997).

RN [11]

RP VARIANT LQ1 VAL-341.

RX MEDLINE=98230121; PubMed=9570196;

RA Li H., Chen Q., Moss A.J., Robinson M.H., Denfield S.W., Duff D.,

RA Vincent G.M., Priori S.G., Lehmann M.H., Denfield S.W., Duff D.,

RA Kaine S., Shimizu W., Schwartz P.J., Wang Q., Towbin J.A.;

RT "New mutations in the KVLQ1 potassium channel that cause long-QT

RT syndrome.";

RL Circulation 97:1264-1269(1998).

RN [12]

RP VARIANT LQ1 THR-300.

RX MEDLINE=98303396; PubMed=9641694;

RA Priori S.G., Schwartz P.J., Napolitano C., Bianchi L., Dennis A.,

RA de Fusco M., Brown A.M., Casati G.;

RT "A recessive variant of the Romano-Ward long-QT syndrome?";

RL Circulation 97:2420-2425(1998).

RN [13]

RP VARIANT LQ1 SER-305.

RX MEDLINE=98454341; PubMed=9781056;

RA Neyroud N., Denjoy I., Donger C., Gary F., Villain E., Leenhardt A.,

RA Benali K., Schwartz K., Coumel P., Guicheney P.;

RT "Heterozygous mutation in the pore of potassium channel gene KVLQ1

RT causes an apparently normal phenotype in long QT syndrome.";

RL Eur. J. Hum. Genet. 6:129-133(1998).

RN [14]

RP VARIANTS LQ1 ARG-168; SER-314; CYS-315; ASN-318; PRO-353 & TRP-366.

RX MEDLINE=98360095; PubMed=9693036;

RA Splawski I., Shen J., Timothy K.W., Vincent G.M., Lehmann M.H.,

RA Keating M.T.;

RT "Genomic structure of three long QT syndrome genes: KVLQ1, HERG, and

RT KCNE1.";

RL Genomics 51:86-97(1998).

RN [15]

RP VARIANTS LQ1 ILE-312 AND ASN-317.

RX MEDLINE=98141684; PubMed=9482580;

RA Saarinen K., Swan H., Kainulainen K., Toivonen L., Viitasalo M.,

RA Kontula K.;

RT "Molecular genetics of the long QT syndrome: two novel mutations of

RT the KVLQ1 gene and phenotypic expression of the mutant gene in a

RT large kindred.";

RL Hum. Mutat. 11:158-165(1998).

RN [16]

RP VARIANT LQ1 PHE-339 DEL.

RX MEDLINE=98366466; PubMed=9702906;

RA Ackerman M.J., Schroeder J.J., Berry R., Schald D.J., Porter C.-B.J.,

RA Michels V.V., Thibodeau S.N.;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122563; PubMed=2448635;
 RA Schwarz T.L., Tempel B.L., Papazian D.M., Jan Y.N., Jan L.Y.;
 RT "Multiple potassium-channel components are produced by alternative
 splicing at the Shaker locus in Drosophila.";
 RL Nature 331:137-142(1988).
 RN [2]
 RP SEQUENCE OF 1-349 FROM N.A.
 RC STRAIN-CANTON-S;
 RX MEDLINE=88396413; PubMed=2456921;
 RA Pongs O., Kerschmethyl N., Mueller R., Krah-Jentgens I., Baumann A.,
 RA Kiltz H.H., Canal I., Llamazares S., Ferrus A.;
 RT "Shaker encodes a family of putative potassium channel proteins in
 the nervous system of Drosophila.";
 RL EMBO J. 7:1087-1096(1988).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS ARE PRODUCED BY ALTERNATIVE
 SPLICING.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X07134; CAA30146.1; -
 DR EMBL; X06742; CAA29917.1; -
 DR PIR; S00482; S00482.
 DR PIR; S00508; S00508.
 DR Flybase; FBgn0003380; Sh.
 DR InterPro; IPR000636; -
 DR InterPro; IPR003091; -
 DR Pfam; PF00520; Ion_trans.1.
 DR PRINTS; PR00169; KCHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Alternative splicing; Multigene family.
 FT TRANSMEM 228 246
 FT TRANSMEM 279 300
 FT TRANSMEM 311 332
 FT TRANSMEM 358 382
 FT CARBOHYD 102 102
 FT CARBOHYD 259 259
 FT CARBOHYD 263 263
 FT CARBOHYD 625 625
 SQ SEQUENCE 656 AA; 74316 MW; 8F09B69B6793FEE CRC64;

Query Match 2.4%; Score 139.5; DB 1; Length 656;
 Best Local Similarity 20.8%; Pred. No. 0.093;
 Matches 58; Conservative 55; Mismatches 109; Indels 57; Gaps 8;

OY 104 VLVILFVLSIGSLIYFINS-----DPVSCSSYEDKIP-----IDLVFN 146
 DB 229 VAIISVAVIL-SVIFCLFETPEFKHYKVFNTTGTKIEDEVDIDPFLIETLCI 287
 OY 147 AEFSEYFGLEFMAADKIKFLEMNISIVDIFTPFTISYLL----- 188
 DB 288 IMETFEFLYVFLACPKLNCRDVMNVIDIALIIPYFILTAVVAEEDTLNPKAPVSP 347

OY 189 ----KSNWLGRLRLRLLELPOLLIILRAITSNVSKEKSLIITLSTWTTAG---- 240
 DB 348 ODKSSNQAMSLAILRVIRL-----VRVRIEFLSRHSGLIQILGRTLKASMRLEGLIF 401
 OY 241 --FIHLVENSQDPMWLGKRNQNSISYFESI----YLMATSTSTVGFQDVYAKTSIGFTFM 294
 DB 402 FLFIQVVLSSAVYFPAEAGSEN-SFKRSIPDAFMAVVTMTIVGDMTPVGVWGAIVGS 460
 OY 295 FFTIGSLILFANYIPENVELFANKRKRYTSSYEALGKRF 333
 DB 461 LCAIAGVLTALPVPVIVSNFNYFHRETDQEMQSNF 499

Search completed: October 5, 2001, 12:12:26
 Job time: 568 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2001, 12:04:48 ; Search time 53.76 Seconds
(without alignments)
1565.716 Million cell updates/sec

Title: US-09-176-664-16

Perfect score: 5722

Sequence: 1 MFQTKLRNMTWEDLPKMSCT.....CIHQSLTSLRSLPLSLK 1105

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3717.5	65.0	1112	2 T42383	probable calcium-a
2	2355.5	41.2	1113	2 S62904	calcium-regulated
3	2350	41.1	1196	2 A48206	calcium-activated
4	2338	40.9	1184	2 I49017	calcium-activated
5	2002.5	35.0	1175	2 JH0697	potassium channel
6	1995	34.9	1184	2 A39800	calcium-activated
7	1873.5	32.7	985	2 T27083	hypothetical prote
8	1538.5	26.9	609	2 I38586	calcium-activated
9	451	7.9	1237	2 T46609	calcium-activated
10	362	6.3	1107	2 T20578	hypothetical prote
11	361	6.3	1119	2 T20577	hypothetical prote
12	316.5	5.5	1017	2 T02865	calcium activated
13	270	4.7	1159	2 T02865	hypothetical prote
14	216.5	3.8	209	2 C64317	hypothetical prote
15	209.5	3.7	455	2 A70461	potassium channel
16	170	3.0	280	2 C82490	probable potassium
17	163.5	2.9	297	2 A82682	ion transporter Xf
18	159	2.8	283	2 B83459	probable potassium
19	158.5	2.8	853	1 CHRTD1	potassium channel
20	158.5	2.8	857	2 I56529	potassium channel
21	158.5	2.8	858	2 S31761	potassium channel
22	158	2.8	802	2 JH0595	potassium channel
23	157.5	2.8	375	2 E70011	potassium channel
24	152	2.7	280	2 E75470	probable ion trans
25	151	2.6	336	2 H69069	potassium channel
26	150.5	2.6	887	2 T03939	potassium channel
27	149.5	2.6	845	2 T07052	probable potassium
28	149	2.6	460	2 T27759	hypothetical prote
29	147.5	2.6	924	2 B41359	potassium channel

30	147	2.6	499	2 I77466	potassium channel
31	147	2.6	807	2 T12177	potassium channel
32	147	2.6	838	2 S23606	potassium channel
33	147	2.6	857	2 S62694	potassium channel
34	146	2.6	630	2 JU0271	voltage-sensitive
35	146	2.6	924	2 S12746	potassium channel
36	145	2.5	787	2 S68699	potassium channel
37	144	2.5	499	2 I84204	potassium channel
38	144	2.5	499	2 A33814	potassium channel
39	144	2.5	1017	2 T31354	potassium channel
40	143.5	2.5	295	2 C72692	probable potassium
41	143.5	2.5	343	2 D64469	potassium channel
42	143.5	2.5	528	2 T34417	delayed rectifier
43	143	2.5	476	2 S21144	potassium channel
44	143	2.5	499	2 A48672	delayed rectifier
45	139.5	2.4	617	2 T23082	hypothetical prote

ALIGNMENTS

Query Match	Best Local Similarity	Score	Pred. No.	Length
Matches 729; Conservative 119; Mismatches 190; Indels 19; Gaps 5;	65.0%	3717.5;	DB 2;	1112;
1 MFQTKLRNMTWEDLPKMSCTTEIOAFLISFVFSGILLIFRLTMRVKKQITKG 60				
1 MSQILDSLNKQELTERTCTEIOAFLISLATPFGILLIFRLTMRVKKQITKG 60				
61 TGIILFTSGTARSHVRLHFOGFRDHIEMLSAQTFVGQVLIVFVLSIGSLTY 120				
61 PGRLTELFSSRRIRANPLRKLTFHGVFORIEMLLSAQTFVGQVLIVFVLSIGSLTY 120				
121 FINSADPVGSSSYEDKRIPIIDIVNAFFSFYFGIRFMAADKIKFWMENSIYDIFIP 180				
121 FINSADPVGSSSYEDKRIPIIDIVNAFFSFYFGIRFMAADKIKFWMENSIYDIFIP 180				
121 FINSADPVGSSSYEDKRIPIIDIVNAFFSFYFGIRFMAADKIKFWMENSIYDIFIP 180				
181 PTFISYVLLKSNMGLRFLRALRLLEPQIILRAIKRNSVKKSKLSIISTWFTAG 240				
181 PTFISYVLLKSNMGLRFLRALRLLEPQIILRAIKRNSVKKSKLSIISTWFTAG 240				
241 FLHVENSGDPLMGRNSQTSYFESIYLVATMSTVGFQGVVAKTSIGRIFIYFTLGS 300				
241 FLHVENSGDPLMGRNSQTSYFESIYLVATMSTVGFQGVVAKTSIGRIFIYFTLGS 300				
301 LILFANITPEWELFANRKRRTSSVEALGKKFTYVGCNTIVDSVTARFLNDKSGEI 360				
301 LILFANITPEWELFANRKRRTSSVEALGKKFTYVGCNTIVDSVTARFLNDKSGEI 360				
361 NTEIVFLGETPPSELETETIFKCYLAVTFTIGSAMKWMEDLRVAVESAEACLIITANPLCS 420				


```
Db 392 TLEESVNFKDLFHKDRDVNVEIVFLHNI SPNLELEALFKRHFVTOVEFQGSVLPHDI 451
Oy 401 RRAVASEACILIANPLCSDHAEDISIKNIMRYLSIKNTDSTRIITIOLOSHNKYLK 460
Db 452 ARKISSADACILANKYCADPDPAEDASINMYISIKNHPKRIITOMLOYNKHLNL 511
Oy 461 ISMNMDTGNIIICFAELKLGFAOGLVPGICTFLLSFEVONKKVMPKQTKHFLNS 520
Db 512 ISMNKKEGDDALCLAEKLGFAOGLVPGICTFLLSFEVONKKVMPKQTKHFLNS 571
Oy 521 MNKILTOPLSDDFAGMSPEVARLCFLMKYLLLIIEKSLFTDQFC--GLILNPPQV 578
Db 572 VSNEMTEYLSSAFGLSPPTVCELCFKLMLAIEKXSNRESRRKRILINGNHL 631
Oy 579 RIRKNTLGRFIAETPKDVRALFECVCHDDVEFIPELLINCGCKSRROHITVPSYRK 638
Db 632 KIOEGTLGFINSDAKEVRAFEYKACCHDDYTDPRKIKKCGC--RLDEQEPFLSPKK 669
Oy 639 KCLKGISSRISGQDSPRVASSTSSISNFTRTLQHD-----VEQSDQLDSS 686
Db 690 K-----QHNCGMRNSP-----NTSPKLMRHPDLPILPNDQIDNMDSNVKKYDST 733
Oy 687 GMEHCKPPTSLDKVTLKRTGSKSKYKFRNHIIVACYEGDAHSAPGLNFYMPILASNYTK 746
Db 734 GMEHCKAPEIEKIVILTRSEAAATVLSGHVVCIFEDVSALGLNLVPLASNFHYH 793
Oy 747 ELKDIVETSLDYLOREMFELRNFOIYILPGCALYSGLDGLAHANIEQCSMCALVSPPOP 806
Db 794 ELKHIVFVGSIEYELKREWEFTLHNFPRVSLIPGTPLSRADLRANINMLCMCVILSNQNN 853
Oy 807 SSONIIVDTFALIMATLITTSLOID-----SSDPSPVSE--ETPG 845
Db 854 IDDTSLQDEKICILASLNKSKQFDSIGVLOANSOGFTPPGMDRSSPDMSPVHMLRQPS 913
Oy 846 YTNCHN-----EKSGCKRVPLTELKNSNHFIEQLGLEGSLQ 885
Db 914 ITTGVAIPITTELAKRGKPLPVSVNDEKNSGTHIMTELVDNTNQFDO--DDDDP 970
Oy 886 ETNLHLSTAFTGVTFSSFLDSLATAFYNYHVELLOMLTVGVSQLEOHLDKYV 945
Db 971 DRELVTLOPFACGTAFVAVSVLDSMSATYFNDNIIILITVLTGATPELEALIAENML 1030
Oy 946 GVADECTSLSRNCKGLLSLHETILSDVNPRTFQGLFCGSLDFGLVGLYRTID 1005
Db 1031 RGVSTPOTLARNRCRAVQALLDGPFPADLDGCGYGLFKALTYNMLCFGIYLRND 1090
Oy 1006 EELNPE--NKRFFVTRPANEFKLPDVFCAIPFSTACYKRNEEFSLOKSYEIVNKAS 1063
Db 1091 AHLSTPSQCTKRYVITNPRYEFELVPTDLIFCLMQF-----DHNAQSRASLSHS 1141
Oy 1064 OTTEDTFRHKLSHPL 1079
Db 1142 HSSQSSSKSSSVHSI 1157

RESULT 5
JH0697
C:Species: Drosophila melanogaster
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #texl_change 24-Sep-1998
C:Accession: JH0697
R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
Neuron 9, 209-216, 1992
A:Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A:Reference number: JH0697; MUID:92360298
A:Accession: JH0697
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1175 <ADE>
A:Cross-references: GB:M96840; NID:9157775; PID:9157776
C:Comment: This potassium channel protein is activated by calcium.
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A:Gene: FlyBase:slo
A:Cross-references: FlyBase:FBgn0003429
C:Keywords: alternative splicing; calcium binding; ion channel; potassium channel; tr
F:126-143/Domain: transmembrane #status predicted <TM1>
F:165-186/Domain: transmembrane #status predicted <TM2>
F:196-214/Domain: transmembrane #status predicted <TM3>
F:219-239/Domain: transmembrane #status predicted <TM4>
F:250-271/Domain: transmembrane #status predicted <TM5>
F:761-772/Domain: calcium binding #status predicted <CAL>

Query Match 35.0%; Score 2002.5; DB 2; Length 1175;
Best Local Similarity 38.7%; Pred. No. 26-132;
Matches 434; Conservative 188; Mismatches 356; Indels 143; Gaps 17;

Oy 27 FILSSVTFPSGILITLIPLI-----RSVKKQIILKGTIILE 66
Db 52 FILSSVTFPLAGLVLLVLMFAFAFVCCCKREPDLPDPKOEKASRNKQEFEGT----- 106
Oy 67 LFTSGTIANSHVSLHFOGQFRDIEMLSAQTFVGQVILVFLVSLIGSLIYFTIN-SA 125
Db 107 -----FMTEAKDMAGELISGOTTGRILVVLVFLISLISLIIYFDASS 150
Oy 126 DPVGSCTSYEDK-TIPIDLVNFAFESFYGLRMAADDKTKFLEMNSIYDITIPPTFI 184
Db 151 EEVERQOKSNNTTQOIDLAFNIFEMVYFIRPIAASDKLMFLMWYSFVDYETIPPSFY 210
Oy 185 SYLKSNMGLRPLRLRLLELPOLIOILRAIKTSNVKPSKLSLITLSTWTFPAAGFIHL 244
Db 211 SYLDWTGIRLRLRLRLMTVPDIIOQLVNLTKTSSSIRLAQVLSFISWLTAAQIHL 270
Oy 245 VENSQDPMWLGKRNQNSIYSESTIYLVMTTSTVGFQDVVAKTSLGRTFIWFTLGLSLF 304
Db 271 LENSQDP-LDFDNARLSWTVCYFLITVMTSTVGYDVCETVGLFVFLVGLAMF 329
Oy 305 ANTPRMVELFANKRKYTSYELKGRKFTVCGNTDVSTFNLNPLRDKGELINTEL 364
Db 330 ASSIPETIELVSGNKYTGGBELKREHGRHIVVCGHTTESVSHFLDFLHEDREDVVEV 389
Oy 365 VFLEGPSTLELTETIFKCYLAATTFYSGSNMKWEDLRVAVEASEACILIANPLCSDSNA 424
Db 390 VFLEHRPRDLELGLRKHTFTVEFFQGTIMNPIDQRYKHADACIVLANKYCODPDA 449
Oy 425 EDISINRYLSIKNDSTRIITIOLOSHNKYVLPKIPSNMMDTGNIIICFAELKGFIA 484
Db 450 EDANIMRYLSIKNSDDIRVILQMOYHNKAYLILPSPMDKQGDVLCIAELKGFIA 509
Oy 485 OGCLVPGICTFPLSLFVEONKKVMP-KOTWKKHFLMSMKKILTORLSDDFAGMSPEVA 543
Db 510 QSCLAGFSTTMANLFAHMSFKTSPMQSWTNDYLGCTGHEMTETLSLPTFGIIPAQAT 569
Oy 544 RLCEFLMYLLAIEYKSLFTDQFCGLILNPPQVIRKNTLQFFIAETPKDVRALFYC 603
Db 570 ELCEFKILLLLAIEIKGA-EEGADSKISINPRGAIQANTQGFIAQSDAEVKRAMFVC 628
Oy 604 SYCHDVFTIPELITNCGK-----SRKQHTIV----- 631
Db 629 KACHEDIKDETLKKCKKNLTGVOPRSKFPDLDGIRDRDEDTLNLNRNRRPRTGNGTG 688
Oy 632 -----PSYRKMKCLKGISRSISGO--DSPRVASSTSSISNFTT-- 669
Db 689 GHHNMNTAAAAAAGAKQYKVKVPTV-IVSRQYEGOVISQVNRPTSRSSSGICTON 747
Oy 670 -----RTLQHDVEQSDQLDSSGMEHCKPPTSLDKVTLKRTGSKYKFRNH 715
Db 748 QNGGVSLPAGIADDSKDPDFEKTEMKYDSTGFMHSPAKSLDEDCLDRNQAMVPLNCH 807
Oy 716 IVACYFGDAHSAPMGILRNVMPLRASNYTRKELDIVTIGSLDYLOREKRFILNFOIYI 775
Db 808 VVVCLEFADDDSLIGLRNLVMPILRASNFHYHELKHVIVIGSVYDIRREKMKQNLPIKISV 867
Oy 776 LPGCALYSGDLHAANIEQCSMCALVSPPOPSSNQVLDTEALIMATLITTSLOID----- 830
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Db 868 LNCSPSLRADLRVAVNVLCDMCCILSAKVPNDPDLADKREAILASINIKAMFEDDTIGV 927
 QY 831 -----SSSDPSVSEETPGYTNHNEKSNCRKVPILTELKPNINHIETOLGG 879
 Db 928 LSGRGPFDLNSATAGSPYVQRR-GSVYGAN-----VPMITELVNDGNVQFLDQ--- 976
 QY 880 LEGSLAETNLHLSTAFSTGTGVSSSSFLDSLATAFYVHYVHLELLQMLVTGVSQDLBOHL 939
 Db 977 DDDDDPDTLEYLTQPFACGTAFAVSVLDSLMTSTYFNQNLMLTLRSLITGGAPELELIL 1036
 QY 940 DKDKYVGVADSCSTLSGKRNCKIGLLSHETILSDVNPRTGQLCGSLDFGLICV 999
 Db 1037 AEGAGLNGYSTVESLNRRCRGOISLYDGLAOPGECGRYDDELVAALSKYMLCIG 1096
 QY 1000 LYRLID-EELNPNKRFVITRPAHEKLLPSDLVFCALPF 1039
 Db 1097 LYRFRDTSSSCDASSKRYVITNPPDDELPTDOVFLVLMQF 1137

RESULT 6

A39800
 Calcium-activated potassium channel, composite form - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 01-Dec-2000
 C:Accession: A39800; PS0444
 R:Atkinson, N.S.; Robertson, G.A.; Ganetzky, B.
 Science 253, 551-555, 1991
 A:Title: A component of calcium-activated potassium channels encoded by the Drosophila
 A:Reference number: A39800; MIM:91313401
 A:Accession: A39800
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1184 <ATK>
 A:Cross-references: GB:M69053; NID:q158468; PID:q158469
 R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
 Neuron 9, 209-216, 1992
 A:Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
 A:Reference number: JH0697; MIM:92360298
 A:Accession: PS0444
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 633-679 <ADE>
 C:Comment: This potassium channel is activated by calcium.
 C:Genetics:
 A:Gene: FlyBase:slo
 A:Cross-references: FlyBase:Fgn0003429
 C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 34.9%; Score 1995; DB 2: Length 1184;
 Best Local Similarity 38.0%; Pred. No. 6.9e-132;
 Matches 436; Conservative 189; Mismatches 353; Indels 168; Gaps 18;

QY 27 FILSSFTVFFSGLLILFLRI-----WRSVKWQIINKGTGIIILE 66
 Db 36 FILSSITFLAGLLLVLMRAFAVCCRKPELDGPNPKQEKASNNKQFEET----- 90
 QY 67 LFTSSTIARSHVRSKLNQGGFRDHEMLSAQTFVGQVLYLVVLSIGSLIIFIN-SA 125
 Db 91 -----FMTEKKDWAGELISQTTTGRLVLLVYLISASLIIFVYASS 134
 QY 126 DPVSGSSSYEDK-TIPIDLVENAFSFFYGLRFMAADDKIKFEMLEMSIVDIETPTPI 184
 Db 135 EEVRRCKMNSNITQDIDLAENIFWFYFIRFASDKMLFEMLSFYDYFTIPSPFV 194
 QY 185 SYVUKSNMGLRFLRALRLLEPOILOILRAIKTSNVSKSLIILSTWTAAGFTHL 244
 Db 195 SIYLDRTWIGIRFLRALRLMTVPIQLYLWLKSSSIRLAQLVISIYVWLTAAGIHL 254
 QY 245 VENSGDGMWLGKRNQNTSYFESITLVMAWTSTVGEGVAVAKTSGRTFIMFTLSLILF 304
 Db 255 LENSGBP-LDFDNHRLSIWTVCYFLIVTWSTVGVDYCTVLGRTFLVFFLLVGLAMF 313

QY 305 ANYIPEWVELFANKRKYTSSYEALGKRFIVYVGNITVDVTAFLRNLDRKSGEINTEI 364
 Db 314 ASSIPEITELVSGSKNGGELKREKGRHLYVCHIEVSYHKLQFLEHREDRDVDEV 373
 QY 365 VFLEGTPPSLELETIFECYLAATTFISGSAMKEDLRVAVESAECLLIANPLCSDSHA 424
 Db 374 VFLEHRPPDELELEGFRRHFTVVEFFQGTIMNPDLORVYVHEADCLVLANKCCODPDA 433
 QY 425 EDSINIRVSTIKKYDSTFTIIOILSHNKVYLPKIPSNMWDGDNIIICPAELKGFIA 484
 Db 434 EDANIMKRVSTIKKYSDDIRVYIQLQYHNKAVLNIIPSDMKOGDDVITCLAEKLGLFIA 493
 QY 485 QGCLVPLGCTFLSLFVEONKQVMP-KQVWKHFLNSMKKILTORLSDDFACMSPEVA 543
 Db 494 QSCLAPEFTSMANLFLMRSPKTSPOMSQWNTNDLRTGCMENYETISLPFFIGIPFQAT 553
 QY 544 RLCPFLKMYLLIAIEYVSLTFDGFGLILNPPQVRIKNTLGFETAPKDVRAALFYC 603
 Db 554 ELCPSKLKLILLAEIKGA-EGADSKISINPRGAKIQANTQGFIIQSADEVKRAMFYC 612
 QY 604 SVCHDDVFIEPLTNCCKS-----RSR-----OHITVPS----- 633
 Db 613 KACHEIDIKDELTKCKCKMLVQPRSKFDOLDENHAPFTPELPKRVNHRGVSVDI 672
 QY 634 -----VKRMKCKLGISSR 647
 Db 673 TRQREDTNLNRNVRNRNGTNGTGMHNNNTAAAAAAGKQVNNKAKPTV-NYSRQ 731
 QY 648 ISGO-DSPPRYASTSSISNFTT-----RTLOHDVQDSQDLOSSGMFH 690
 Db 732 VEGGVISPSQYNRPRTSSSGTGNONGVSLPAGIADDSKDFPFKTEKKYDSTGMFH 791
 QY 691 WCKRTSIDKWTIKRTGSKKFRNHIVACYVGDHSAHPKGLRNRYMLASNTYRKLKD 750
 Db 792 WSPAKSLIEDCILDNQAAKTVLNGHVYVCLFADDSPLIGRLNLYMLRASNFHYHKLK 851
 QY 751 IVFGISLDYLOREWRFLRNFPQIYILPGCALYSDDLAAANIEQSCMACVSPRPQSSNQ 810
 Db 852 VVIYGSVDYIRREKMKLQNPCKISVNLGSPSLSRADLRVAVNNLCDKCCILSAKPPSDDP 911
 QY 811 TLVDTEAIMATLTIGSLQID-----SSSDPSVSEETPGYTNHNEKS 854
 Db 912 TLADKEAILASLNIAKAMFTDITIGVLSQRGPEFNDLSATAGSPYVQRR-GSVYGAN--- 967
 QY 855 NCRKVPILTELKNSNHFIPQLGCLGSLQETNLHLSTAFSTVSSSFLDSLATAF 914
 Db 968 ---VPMITTELVDNGNVQFLDQ---DDDDPDTLEYLTQPFACGTAFAVSVLDSLMTSTY 1020
 QY 915 YNYHVELLQMLTVGVSSQLEOHLDRKQYGVADSCSTLSGKRNCKIGLLSHETILS 974
 Db 1021 FQNALTLIRSLITGATPELELILAGAGLRGYSVESLSNDRCRVGOISLYDGPLA 1080
 QY 975 DVNPRNTFGQLFCGSLDFFGLICVGLYRIID-EELNPNKRFVITRPAHEKLLPSDLV 1033
 Db 1081 QFGEGCYGDLFVALAKSYGLCIGLYRFRDTSSSCDASSKRYVITNPPDFFSLPTDQV 1140
 QY 1034 FCALPF 1039
 Db 1141 FVLMOF 1146

RESULT 7

T27083
 hypothetical protein Y51A2.19 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 R:McMurray, A.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z20307
 A:Accession: T27083
 A:Status: preliminary; translated from GB/EMBL/DBU
 A:Molecule type: DNA


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Db      316 NGESHVAVYITTTLEEFIDLEEFAPRNO-RIOIVLL--SPAELDQTMMLKIPL 372
      385 --AYTFISGSAMKWDLRVAESAACLIIANPLCSDSHADISIMVLSIKNDST 442
      373 WNNRVHYVRSSLRDDELEANAVATSKACITLSARHNKRVAVDEHTILLSMAIKDAPN 432
      443 TRIIIOLOSHNKVVLPKIPSMWMDGDNITICFAELKLGFIAGCCLVPGCTFLTSLEVE 502
      433 VKQYVOIFRAETRMHI-----EHAEVLICEDDEFYALANNCICPGISTFTLLMHT 484
      503 QNKKVMPKOT--WKK-----HFLNSM--KNKILIQRLSDDFAGNSPEPARCFLKMYLLI 555
      485 SREBEGKSTEPNKKYGFHSGNEMYOIKVODSKFCEYVGSFSTSPFAHKEYGIGLI 544
      556 AIEYKSLFTDGFSG-LILNPPQVRIKNTLGFPIA---ETPRDYRALFYCSVCHDV 610
      545 AVS-----PDGDTSRMKNLNGSHIIQPTDYVYMGLTNESLIDPRKGI---RSQOKRA 596
      611 FIEELLTNGCC-----KSRSHQITVPVSKRMKC-----LKGISRSIGODSPRVS 659
      597 NVASTIANIGTAVADVPRSDKTELVGKKRREKADEIHLIEVEGHVQSSRRPSIAMV 656
      660 STSISNFTTR-----TLQHDVRODSQDQ-----DSSGMFMCKP-----TS 696
      657 TEKIDSSSDDEICDCKRCGPCIOHKLQRTYPOVRTYIGTSNTVCCHMKERRSLCCLK 716
      697 LDKVTLKRTGKS--KYKFRNHIVACVGDASHAPMGLRNFVMPLRASNTYRKELKDIV-- 752
      717 LDKCAHKSATSAHEYOVRNRPIILA--ADRTSSGMYNLVILRAYRVVHDLHPITIL 773
      753 -----FIGSLDYIQREMRFLRNPQIYILPG-----CALYSGDLMANIEQC 794
      774 LELEODSLNDAFLDAISY-----FPDYVMKMGKGNLDCLLRAGVSSAEHVVV 823
      795 SMCAYVSPRPPSSNOTVDTVEAIMATLTIGSLQIDSSSPSPSVSEETPGYINGHNKS 854
      824 KETAVMAEHTADCN-TITIVOKIHRMP----- 851
      855 NCRKVPILTELKPNINHFIE-----QLGLESLQOETNHL-----STAFSTGTV 901
      852 ---RLMITELTHATNMRFQFNPNNAYSLAOSRFEKKEKRSHPMRFLRFAQGV 908
      902 SSSFSLSLATAFYNYHVELLQMLVTVGGVSSOLEHLDKDKYGVADSCSTLSGRNRC 961
      909 SAMMDRLLYOALIKPEVVDVLRLL-----GIDQSDG----- 942
      962 KIGLSLHETILSDVNPRTFGOLF--CGSLDLFGILCYGLYRI-----IDEEEL 1009
      943 --GYLTSFVITSDMLIRN-YGRLYOKLSSV--ADIPIGITRTKKMDTKTYVSLDLOEQ 996
      1010 NPNKRFVITRPAHEKLLPSDLVFCALPSTACYRNEEFSLOKSEIYNKASQTTEDT 1069
      997 CKPFENTEMGRNDMYDVHVRRLINKOTHTLLEGSDKS-QISVVIINPADL----- 1051
      1070 FRHKLSSHPLQLLRHCINOSILTSR 1095
      1052 ---ELESGLVYVIRSPIKDATNAR 1074

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RESULT 11

T20577
 Hypothetical protein F08B12.3a - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T20577
 R: Dobson, R.
 submitted to the EMBL Data Library, November 1995
 A: Reference number: Z19295
 A: Accession: T20577
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-1119 <MIL>

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A: Cross-references: EMBL:Z68104; PIDN:CAA92115.1; GSPDB:GN00028; CESP:F08B12.3a
A: Experimental source: clone F08B12
C: Geneticals:
A: Gene: CESP:F08B12.3a
A: Map position: X
A: Introns: 38/2; 64/1; 112/2; 148/3; 173/3; 201/3; 348/3; 392/2; 452/1; 488/2; 538/2;

Query Match      6.3%; Score 361; DB 2; Length 1119;
Best Local Similarity 20.4%; Pred. No. 5.1e-17;
Matches 228; Conservative 179; Mismatches 424; Indels 286; Gaps 48;

      101 VGOVLVIVLVLST--GSLIYFINSADPVGSCSYEDKTIPIDLVENAFSPYFGLREMA 159
      134 ISMAYTILVEYLSYSGSVRLIN-----IHFLLELTISFPF----- 170
      160 ADDKIRFMLEMNSIVDTFTPR-----PFEISYLYKSNMLGRLRALLELPOLIOI 212
      171 -----TISIF-IPSLTYLVVFLNC-----HLAKGALQAM-----MNDL 204
      213 LRAIKTSNYSVKFSKL--SIILSTWETAAGT-HLVENSQDPMKGRNSQNIYESIY 268
      205 NRSFSISSALFQQLLLEFVLACLIFTGMCSTIEHLQIRANG-----KRIDLFTSEY 255
      269 LVNATTSTVGFGDVAKTSLGRTFIMEFTLGSLLIPANYPENVELFANKRKYTSYAL 328
      256 FVMATFESTVGDMYPRDYMASQLCVLLICVALGLIPKQDELQGVTFSEKSGTGFSSW 315
      329 KG--KKFIVYCGNITVDSVAFILRNLFRDSSGEINIEIVLGFTPSLEET--IFRCYL 384
      316 NGESHVAVYITTTLEEFIDLEEFAPRNO-RIOIVLL--SPAELDQTMMLKIPL 372
      385 --AYTFISGSAMKWDLRVAESAACLIIANPLCSDSHADISIMVLSIKNDST 442
      373 WNNRVHYVRSSLRDDELEANAVATSKACITLSARHNKRVAVDEHTILLSMAIKDAPN 432
      443 TRIIIOLOSHNKVVLPKIPSMWMDGDNITICFAELKLGFIAGCCLVPGCTFLTSLEVE 502
      433 VKQYVOIFRAETRMHI-----EHAEVLICEDDEFYALANNCICPGISTFTLLMHT 484
      503 QNKKVMPKOT--WKK-----HFLNSM--KNKILIQRLSDDFAGNSPEPARCFLKMYLLI 555
      485 SREBEGKSTEPNKKYGFHSGNEMYOIKVODSKFCEYVGSFSTSPFAHKEYGIGLI 544
      556 AIEYKSLFTDGFSG-LILNPPQVRIKNTLGFPIA---ETPRDYRALFYCSVCHDV 610
      545 AVS-----PDGDTSRMKNLNGSHIIQPTDYVYMGLTNESLIDPRKGI---RSQOKRA 596
      611 FIEELLTNGCC-----KSRSHQITVPVSKRMKC-----LKGISRSIGODSPRVS 659
      597 NVASTIANIGTAVADVPRSDKTELVGKKRREKADEIHLIEVEGHVQSSRRPSIAMV 656
      660 STSISNFTTR-----TLQHDVRODSQDQ-----DSSGMFMCKP-----TS 696
      657 TEKIDSSSDDEICDCKRCGPCIOHKLQRTYPOVRTYIGTSNTVCCHMKERRSLCCLK 716
      697 LDKVTLKRTGKS--KYKFRNHIVACVGDASHAPMGLRNFVMPLRASNTYRKELKDIV-- 752
      717 LDKCAHKSATSAHEYOVRNRPIILA--ADRTSSGMYNLVILRAYRVVHDLHPITIL 773
      753 -----FIGSLDYIQREMRFLRNPQIYILPG-----CALYSGDLMANIEQC 794
      774 LELEODSLNDAFLDAISY-----FPDYVMKMGKGNLDCLLRAGVSSAEHVVV 823
      795 SMCAYVSPRPPSSNOTVDTVEAIMATLTIGSLQIDSSSPSPSVSEETPGYINGHNKS 854
      824 KETAVMAEHTADCN-TITIVOKIHRMP----- 851
      855 NCRKVPILTELKPNINHFIE-----QLGLESLQOETNHL-----STAFSTGTV 901
      852 ---RLMITELTHATNMRFQFNPNNAYSLAOSRFEKKEKRSHPMRFLRFAQGV 908
      902 SSSFSLSLATAFYNYHVELLQMLVTVGGVSSOLEHLDKDKYGVADSCSTLSGRNRC 961

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Db 509 SANMLDRLLYGAIIRKPFVVDLVRLL-----GIDQHS DG----- 942
Oy 962 KLGLSLHETILSDVNPNTGOLF--CGSLDFGLICVGLYRI--IDEE---ELNPE 1012
Db 943 --GLTSEFVITSDLLMIRN-YGRLYOKLCSSV---ADIPGIFRKKMDTFTVSLDLOEQ 996
Oy 1013 NKRRVTRPRA-----NEFKLLP-SDLVFCALPSTGACYNKEEFSLOK---SYEI 1058
Db 997 CKDENTENMGKNDKMYDVKRNMRLNLIKDTHTFNMWKYASCRSRVIEGSDKQSISYI 1056
Oy 1059 VNKAQOTEDTFRHKLSSHPILLRHCIOHSILTSR 1095
Db 1057 INPADL-----ELESGLDIYVIRSPIDRKDATNAR 1086

RESULT 12
T02865
calcium activated potassium channel CACK1 [Imported] - Leishmania major (strain Friedlin
C:Species: Leishmania major
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C:Accession: E81464; T02865
R:Myler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A:Reference number: A81455; MUID:99178987
A:Accession: E81464
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1017 <PVL>
A:Cross-references: GB:AE001274; NID:93264850; PIDN:AC24688.1; PID:93002487; GSPDB:GNOC
A:Experimental source: strain MHOM/IL/81/Friedlin
A:Genetics:
A:Gene: CACK1
A:Map position: 1

Query Match 5.5%; Score 316.5; DB 2; Length 1017;
Best Local Similarity 19.9%; Pred. No. 6e-14;
Matches 204; Conservative 154; Mismatches 437; Indels 229; Gaps 39;

Oy 141 IDLVFN-AFESFYGLRPMADDK--IKFWLEMSIVDIFPTPTF---ISYYLKSNNLG 194
Db 96 VELVLSIFFLAWGLFFEPEDKAYLISWL---SLVNAMTISPIVIGIGALKDSSWS 152
Oy 195 LRFRLAR-----LLELPOLQLLRKITSNVKFSKLSIISTWTFAGFIHL 244
Db 153 VWVPYLVVWMLCDCLSVLIDYPOIARHTPEKWRMRYFIRLFVVC---TCVGTQOI 208
Oy 245 VENSQDPLKGRNSQNIYSFESIYVMATTSVFGDVAVATSLGRTFIMEFTLSLLE 304
Db 209 VESCSGVY-----VDLYDSLYIIVAFNITIGRGDTAFTTPARIMIAFIYIGICFF 260
Oy 305 ANYID-EMVELPANKRRTYSYEA-----LKGK--FIVYCGNITVDSYTAFLRNF 353
Db 261 --LPLFRLSVIARSOHLMTFSGGSASWLRGMKHPHYVICQFSDSELLRNFY 317
Oy 354 RDKSGEINTETVFLG--ETPPSELETIFKCYLATTFISGAMKWEELRRAVASEANC 411
Db 318 AGMKRYIDTCIYLAPEESHSPREVRLAANLPMWLGKRVTLVAGPAPKDLRAKADADAI 377
Oy 412 LIANPLCSDSHADISNIMRVLSIKNYDSTRIIQLQSHNKYYLPRISWMDTGDN 471
Db 378 FLFGGRS-STAYVDYTIILASVANSYD---RNLPQHLHLRNTVQOISY---AAS 429
Oy 472 IICAEELKGLTACGLVPGICTFLTSL--FVEQNKVMPKQTKKHFLSNMKNKILIQ 528
Db 430 VLEVERIHLHLGLISMARPGVPLVNLRTYESLPDITLSRHVWEQYEYSIRNDMGL 489
Oy 529 RLSDQFAGMSPEVARLCEFLKMYLLLIIEKSLFTDGFGLILNPPQVIRKNTLGEF 588
Db 490 ELPDLRGRREFVLRARSEFEDVDTLIGILNRSV-----VOLNPRELVNPAKKLI--L 540
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Oy 589 IAETPKDVRRLALFYCSYCHDDVFIPELIT-----NCGCKSRSRHOITVPSVKRMKCL 641
Db 541 IAKTKVAQADATDAIARHEOTFGEMLAAPDPDEHDAKRRARSRRLVILBRSSSSSS 600
Oy 642 KGISRSISGQDPPR-----VSASTSSISNFTTLOHDVE----- 677
Db 601 SGVDQDVEDRNGAPRGDRMPROTAVHSASRPATPTATTIDSQRTQVPRPAAAAALEN 660
Oy 678 -----QDSDQDSSGMFMKCPISLDKY-----TLKR 704
Db 661 GNGLARAPPVSVSLHPSGSSIAAEGSSGDEFDARSIVAAASPBPSSMRAPVNSEALVR 720
Oy 705 TGKSKYKFRNHIVACVFSDAASAPWGLR-----NFVMPLRASNTYRKL- 748
Db 721 IDDA-FDLENHFPVVDLSSAKAKDESSRYAOEAVNTAAHDIPIHTVMPVRA-TPANDV 778
Oy 749 --KDIVEIGSLDYLRQREPLRNPQIYILPGCALYSGLDHAANI EOCSSMCVAVLSPPO 805
Db 779 LLTNDVSEFPYLDYVWSVHRDASNPVKYI--SGCGLNTADLRRCMLERCACGVYAGDV 837
Oy 806 PSSNQTIVDTAIAATLTIGSLQIDSSDPSPSYSEETPGYTNNGINENKRPVIL--- 862
Db 838 SRSGST-----SAMSMLTVLSINETLHGIRPAFPVVELEGAN-----LPLFPPH 882
Oy 863 --TELKNPSNIHFEQGLGEGSLQETNHLSTAFSTGYFSSSFLDLSLATAFYNYHV 919
Db 883 AEDLRKTRKAEIDFY-----YEPN-----FITGNVSRMLPLPALQRTYFMEEF 926
Oy 920 LELLQMLVTGGVSSQLEQHLDKKYYGVADSCSTLSGRNCKLGLSLHETIISDVNPR 979
Db 927 IDVMVLTLSGHAPD-----TPALA--RLPLSLFOAEIQTYEDV--- 962
Oy 980 NTFQGLFCGSLDRCILCVGLY-RIIDEEELNPEKKREVIRPANEFLLP-----SDLVF 1034
Db 963 ---VVYCL--FGYLPALQRIYDVNPSINQRCVLTNPP--RALPYNOQTDLF 1012

Oy 1035 CAIP 1038
Db 1013 YTP 1016

RESULT 13
T02866
hypotheical protein CACK2 [Imported] - Leishmania major (strain Friedlin)
C:Species: Leishmania major
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C:Accession: E81464; T02866
R:Myler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protei
A:Reference number: A81455; MUID:99178987
A:Accession: E81464
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1159 <PVL>
A:Cross-references: GB:AE001274; NID:93264850; PIDN:AC24688.1; PID:93006218; GSPDB:G
A:Experimental source: strain MHOM/IL/81/Friedlin
A:Genetics:
A:Gene: CACK2
A:Map position: 1

Query Match 4.7%; Score 270; DB 2; Length 1159;
Best Local Similarity 16.5%; Pred. No. 1.4e-10;
Matches 194; Conservative 178; Mismatches 442; Indels 360; Gaps 38;

Oy 63 ILELETSQTARS-----HVRSLHFOGFRDHIMLSAQTFVGOVIVLVLSIGSL 117
Db 139 ILLILCNVGLAARAGIYLVHQNAAVHTADWR---EFDGICGFIAIEVLLSVFMASSWLSL 195
Oy 118 II-----YFINSADPYGSCSYEDKTIPIDLVNAFFSYFGLRPMADDKIKFWLEM 170
Db 196 LAVEAKKNNVYVLAARSLSNNYLS-----GWWLL 223
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[illegible]

PS Claim 1; Page 79; 93pp; English.
XX
CC The invention relates to a voltage-gated, pH sensitive potassium channel
CC S103, expressed in spermatoocytes. S103 has, as a monomer, calculated
CC molecular weight 120-156 kD; has unit conductance (as a functional
CC tetramer, when expressed in Xenopus oocytes) of 80-120 pS; has increased
CC activity at intracellular pH above about 7.1 and binds specifically to
CC polyclonal antibodies against sequences shown in AAY13437, AAY13438,
CC AAY13442, and AAY13443. S103 is involved in sperm capacitation and/or the
CC acrosome reaction, essential steps in fertilization. S103, and the
CC nucleic acid encoding it, are used to identify specific inhibitors and
CC activators (potentially useful for treating infertility and as
CC contraceptives), also for studying sperm physiology in vitro.
CC S103-specific antibodies are used for diagnostic detection of S103
CC expression. S103, as part of a chimera with another channel protein, can
CC be used as a reporter for measuring changes in potassium concentration,
CC current flow, ion flux, etc. Fragments of S103 nucleic acid are useful as
CC probes for identifying homologs, variants and mutants associated with
CC disease; to detect S103-related mRNA or protein; for chromosomal
CC localization; in gene therapy; for identifying potential modulators; to
CC measure up-regulation of S103 in drug screening assays and for production
CC of recombinant S103 protein. The present sequence represents the amino
CC acid sequence of hS103-1.
XX
XX

Sequence 1105 AA:

Query Match 100.0%; Score 5722; DB 20; Length 1105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTGKLRFNEMEDLPKMSCTTEIOAFLISFPTFSGLLILILFRLMSVKKKQIING 60
DB 1 MGTGKLRFNEMEDLPKMSCTTEIOAFLISFPTFSGLLILILFRLMSVKKKQIING 60
QY 61 TGIILEFTSGTARSHVRSLSHFGQFRDHEMLLSAQFVGVLVILVLSIGSLIIT 120
DB 61 TGIILEFTSGTARSHVRSLSHFGQFRDHEMLLSAQFVGVLVILVLSIGSLIIT 120
QY 121 FINSADPVGSCSSYEDKTIPIDLVFNAFSFFYGLRPMADDKIKFWLENNSTVDIETIP 180
DB 121 FINSADPVGSCSSYEDKTIPIDLVFNAFSFFYGLRPMADDKIKFWLENNSTVDIETIP 180
QY 181 PFTISYVLSNMGLRFLRLRLLELPQIILRAIKTSNVSKVSKLSTIISTWPTAAG 240
DB 181 PFTISYVLSNMGLRFLRLRLLELPQIILRAIKTSNVSKVSKLSTIISTWPTAAG 240
QY 241 FRIHVENSGDPMILKGRNSONISYFESTIYLVMTTSTVGFDDVAKTSLGRTFMPTIGS 300
DB 241 FRIHVENSGDPMILKGRNSONISYFESTIYLVMTTSTVGFDDVAKTSLGRTFMPTIGS 300
QY 301 LILFANYIPBMVELFANKRRKVTSSYEALKGKPIVCGNITVDVTAFLRNPLRDKSGEI 360
DB 301 LILFANYIPBMVELFANKRRKVTSSYEALKGKPIVCGNITVDVTAFLRNPLRDKSGEI 360
QY 361 NRTIVFLGFTPPSLELETFKCYLATTTTSSGAMKWEDEARRAVESAECILIANPLCS 420
DB 361 NRTIVFLGFTPPSLELETFKCYLATTTTSSGAMKWEDEARRAVESAECILIANPLCS 420
QY 421 DSHAEDISNIMRYLSIKNDVSTRIIOLIOSHNKYVLPKIPSMNMDGNTIICPFLKL 480
DB 421 DSHAEDISNIMRYLSIKNDVSTRIIOLIOSHNKYVLPKIPSMNMDGNTIICPFLKL 480
QY 481 GFLAOGCLVPGICTFLTSLFVEONKRVMPKOTWKKHFLNSMKKKILTORLSDFAGMSFP 540
DB 481 GFLAOGCLVPGICTFLTSLFVEONKRVMPKOTWKKHFLNSMKKKILTORLSDFAGMSFP 540
QY 541 EVARLCEFLKMYLLILAIERKSLFTDGCGLIAPPPOVRIKKTFLGFFIAETPKDVRRL 600
DB 541 EVARLCEFLKMYLLILAIERKSLFTDGCGLIAPPPOVRIKKTFLGFFIAETPKDVRRL 600
QY 601 FYGVSVHDDVFIPELITNGCCRSRSHITVPSVKRMKKCLKGISRISSODSPRVSAS 660
DB 601 FYGVSVHDDVFIPELITNGCCRSRSHITVPSVKRMKKCLKGISRISSODSPRVSAS 660

DB 601 FYGVSVHDDVFIPELITNGCCRSRSHITVPSVKRMKKCLKGISRISSODSPRVSAS 660
QY 661 TSSISNFTTRTQHDVEDSDQDSSGMFHWCKPTSLDKVTTLKRTGSKYKFFNNHIVACY 720
DB 661 TSSISNFTTRTQHDVEDSDQDSSGMFHWCKPTSLDKVTTLKRTGSKYKFFNNHIVACY 720
QY 721 FGDASHAPKGLNFWPLRASNTYRKELADIVETIGSLDYLQREWRFLRNFPQIYILPGCA 780
DB 721 FGDASHAPKGLNFWPLRASNTYRKELADIVETIGSLDYLQREWRFLRNFPQIYILPGCA 780
QY 781 LYSGLDILHAANIECCMCAYISPPPOSSNOTVDFEATMATLTIGSLQIDSSDPSPSVS 840
DB 781 LYSGLDILHAANIECCMCAYISPPPOSSNOTVDFEATMATLTIGSLQIDSSDPSPSVS 840
QY 841 EETPGYTNHNEKSNCRKVPILTELKNPSNHPTEQLGEGSLQETNHLSTAFSTGTIV 900
DB 841 EETPGYTNHNEKSNCRKVPILTELKNPSNHPTEQLGEGSLQETNHLSTAFSTGTIV 900
QY 901 FSSSFIDSLATRFYNYHVELLQMLVTGCVSSQLBQHLDDKRYGVADSCISLSGRNR 960
DB 901 FSSSFIDSLATRFYNYHVELLQMLVTGCVSSQLBQHLDDKRYGVADSCISLSGRNR 960
QY 961 CKLGLSLHETIISDVNPRMTFGOLFCGSLDLFGIICVGLYRIIDEELNPEKKRFVTR 1020
DB 961 CKLGLSLHETIISDVNPRMTFGOLFCGSLDLFGIICVGLYRIIDEELNPEKKRFVTR 1020
QY 1021 PANEFKLPBSDLVFCALPSTACRYKNEEFSLOKSYEIVNKAQOTTEDFRRKLSSHPLI 1080
DB 1021 PANEFKLPBSDLVFCALPSTACRYKNEEFSLOKSYEIVNKAQOTTEDFRRKLSSHPLI 1080
QY 1081 QLLRHCIHOSILRSRELPPLFSK 1105
DB 1081 QLLRHCIHOSILRSRELPPLFSK 1105

RESULT 2

AAY13443
ID AAY13443 standard; Protein; 1081 AA.

XX AAY13443;

XX 26-JUL-1999 (first entry)

XX Amino acid sequence of hS103-2.

XX Voltage-gated; pH sensitive; potassium channel; S103; spermatoocyte;

XX sperm capacitation; acrosome reaction; fertilization; infertility;

XX KW contraceptive; sperm physiology; channel protein; gene therapy.

XX Homo sapiens.

XX W09920754-A1.

XX 29-APR-1999.

XX 21-OCT-1998; 98WO-0522321.

XX 27-FEB-1998; 98US-0076172.

XX 22-OCT-1997; 97US-0063138.

XX (UNITW) UNIV WASHINGTON.

XX Salikoff L, Schreiber M, Silvia C;

XX WPI; 1999-326593/27.

XX N-PSDB; AAX55525.

XX Voltage-gated, pH-sensitive potassium channel useful in gene therapy

XX Claim 1; Page 81; 93pp; English.

XX The invention relates to a voltage-gated, pH sensitive potassium channel

XX S103, expressed in spermatoocytes. S103 has, as a monomer, calculated

molecular weight 120-156 kD; has unit conductance (as a functional tetramer, when expressed in *Xenopus* oocytes) of 80-120 pS; has increased activity at intracellular pH above about 7.1 and binds specifically to polyclonal antibodies against sequences shown in AAY13437, AAY13438, CC AAY13442, and AAY13443. SLO3 is involved in sperm capacitation and/or the CC acrosome reaction, essential steps in fertilization. SLO3, and the CC nucleic acid encoding it, are used to identify specific inhibitors and CC activators (potentially useful for treating infertility and as CC contraceptives), also for studying sperm physiology in vitro. CC SLO3-specific antibodies are used for diagnostic detection of SLO3 CC expression. SLO3, as part of a chimera with another channel protein, can CC be used as a reporter for measuring changes in potassium concentration, CC current flow, ion flux, etc. Fragments of SLO3 nucleic acid are useful as CC probes for identifying homologs, variants and mutants associated with CC disease; to detect SLO3-related mRNA or protein; for chromosomal CC localization; in gene therapy; for identifying potential modulators; to CC measure up-regulation of SLO3 in drug screening assays and for production CC of recombinant SLO3 protein. The present sequence represents the amino CC acid sequence of hSLO3-2.

XX Sequence 1081 AA:

Query Match 97.4%; Score 5573; DB 20; Length 1081;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 1081; Conservative 0; Mismatches 0; Indels 24; Gaps 1;

QY 1 MFQTKLNEMTEDI.PKMSCTTETIOAFLTSFVPFSGILLLIPRLIMSVKWKQITIG 60
Db 1 mfgtklnetwedipkmscttelgaafllsftffsgllllllfllwrvskwkqikg 60
QY 61 TGIILLETSGTIRSHVRSI.HFQGFPHIEMLSAQTFVGQVLVLEFVLSGLITY 120
Db 61 tgiillefsgtirsrvsrhngqgdhlemllsagctvgvllvtrvsgslily 120
QY 121 FINSADPVGSSCYEDKTIPIDLVFNAFFSFYFGLREMAADDKIKFWLENNISYDIETIP 180
Db 121 finsadpvgsscyedkripdlvfnaffsfyfglrmaadddkikfwlemnsydfitip 180
QY 181 PFTSYLYKSMWLGRLRALRLLEPOILOILAKITSNSVSKSLSTLSWFTFAG 240
Db 181 pftsylyksmwlgrralrllleppilqlilrakltsnsvskslstlsftfag 240
QY 241 FIHLVENSQDWLGRNSQNSISFEISYLVWATSTVGFQGVNAKTSLGRTIMEFTGS 300
Db 241 fihlvensqdwlgrrnsqnsisfesylvmatstvgfggvnaktsgrtimfctgs 300
QY 301 LILFANYIPEMYELFANKRKYTSSEYALKGRKFTVCGNITVDVTAFLRNLDRKSGEI 360
Db 301 lllfanyipemvelfankrkytsseyalgkklfvvcgnltvdvtaflrnlrdksgei 360
QY 361 NTEIVFGEFPPSLLELIEFKCYLAFTTIFSGSAMKEDLRRVAVESAEALIIANPLCS 420
Db 361 nteivfgefpplsleleifekcyiafttfigsamkredlrrvavesaealilnplcs 420
QY 421 DSHMEDISNIRVLSIKRYDSTTRIIIOILSHNKVYLPKIPSNMWDGDNITICPAELK 480
Db 421 dshmedisnirvlsikrydsttrililqishnkvylpkipsnmwdgdnitlcpaelk 480
QY 481 GFIAOGCLVPLGCTFLSLFVEONKKVMPKQTKWKKHFLNSKNKILTORLSDFAAGSFP 540
Db 481 gfiaogclvpjgctflslfvegnkkvmpkqtkwkhflnsknklltgrlsddfgsagf 540
QY 541 EVARLCLFKMWLLLAIFKSLFTDGFGLLNPPQVRIKKNLIGFIACPKDVRAL 600
Db 541 evarlclfkwmlllaifkslftdgfgllnppqvriknknligfiactpkdvrall 600
QY 601 FYGVCYHADVPELITNCGCKSRROHITVPSYRMKCKLGKISSRSIGDSPRVSAS 660
Db 601 fycvcyhadvpelitnccgcksrrohitypsyrmkcklgkissrsigdsprrvsas 660
QY 661 TSSISNFTTRFLQHDVEDSDQLODSSGFMWCKPSTLDKVTLKRTGSKYKFRNHIVACV 720
Db 661 tssisnfttrflqhdvedsdqloddssgfmwckpstsldkvtlkrtskykfrnhivacv 720

Db 637 tssisnfttrtlqhdvedsdqldssgfmwckpstsldkvtlkrtskykfrnhivacv 696
QY 721 FGDHNSAPMGLRNVMRLASNTYRKELKDLVFGSLDIYQREKRFURNPQIYILPGCA 780
Db 697 fgdhnsapmglrnvmrlasntyrrkelkdvlvfgslldiyqrekrfurnpqiyilpgca 786
QY 781 LYSDDLAAANEQCSMKCAVSPRPQSPSSNOTLVPTETAMATLFGSLQIDSSDPSPSVS 840
Db 757 lysddlnaanlegcsmcavslppqpssnqtlvptetamatlfgslqidssdpspsvs 816
QY 841 EEPGYTNHNEKSNCRKVPILTELKNPSNIHFTEQLGEGSLQETNLHSTAFTSTGV 900
Db 817 eepgytnhnekcncrkvpilteklknpshfiteqlgegsloetnlhstafstgtv 876
QY 901 FSSFLDSLATARYNNHVELLOMLVTGVSQLEBDHDKDKYGVADCTSLSSRN 960
Db 877 fssflslslatarynyhvellomlvtgvsqlebdhdkdkygvadctslssgrn 936
QY 961 CKLGSLSHETILSDVNPRTMFGOLFCSLDLFGITLGVYRIIDEELPENKRPVYTR 1020
Db 937 cklgslshetilsdvnprtmfgoifcsldlfgitlcvlyriideelpenkrpvytr 996
QY 1021 PANEFKLLPSDLVPCAIPFSTACYKRNDEFSLOKSYELVNKASQTTEDTRHKLSSHPLI 1080
Db 997 panefkllpsdlvpcalpftstacykrneefslqksyelvnkassqttedtrfhklshspl 1056
QY 1081 QLRHCHOSTLRSRELTSPSLFSK 1105
Db 1057 qlrhchostlrsreltspslfisk 1081

RESULT 3

AAY13437 standard; Protein: 1112 AA.

XX AAY13437:

DT 26-JUL-1999 (first entry)

DE Mouse SLO3 (mSLO3).

XX Voltage-gated; pH sensitive; potassium channel; SLO3; spermatocyte;
KW sperm capacitation; acrosome reaction; fertilization; infertility;
KM contraceptive; sperm physiology; channel protein; gene therapy.

OS Mus sp.

XX WO9920754-A1.

PD 29-APR-1999.

PF 21-OCT-1998; 98WO-US22321.

PR 27-FEB-1998; 98US-0076172.

PR 22-OCT-1997; 97US-0063138.

PA (UNIW) UNIV WASHINGTON.

PI Salzkof L, Schreiber M, Silvia C;

XX WPI: 1999-326593/27.

DR N-PSDB; AAX55514.

PT voltage-gated, pH-sensitive potassium channel useful in gene therapy

XX Claim 1; Page 77; 93pp; English.

CC The invention relates to a voltage-gated, pH sensitive potassium channel
CC SLO3, expressed in spermatocytes. SLO3 has, as a monomer, calculated
CC molecular weight 120-156 kD; has unit conductance (as a functional
CC tetramer, when expressed in *Xenopus* oocytes) of 80-120 pS; has increased
CC activity at intracellular pH above about 7.1 and binds specifically to
CC polyclonal antibodies against sequences shown in AAY13437, AAY13438,

[illegible]

Dd	715	hefgnhivncvfgdagactlvglrnfymprlraasnytrtqekldvifigsleyfqrewrflrn	774
Oy	770	FPOYLILPGCALYSGDLDHAANIEQCSMCAYLSPPRPSSNQTLVDTETATMTLITGSLDI	829
Dd	775	fpxkhhmpgsalymgdllavneveqscmvllaecrykalssqdlvdteaalmatlnlsqrld	834
Oy	830	DSSSDPSPSVSEENPGVT-IGNHEKSMCRKVPLLTTELKNPSNHHFEOLGEGESLOFTN	888
Dd	835	-tsptpsasxsevhnpssaiafskerktgkqjrpilleteknpsnhtfiegmgldgmkgys	893
Oy	889	LHLTAESTGTVESSFLDSLATAFYNNVLELLQLMLTYGVSSQLDEONLDRKDVYGVA	948
Dd	894	lhstsfstgavfdctldslatsfyhyvvellgmlytgvasemeylvkekykct	953
Oy	949	DSCTSLSGRNCKLGLSLHETILSDVNERNRTFGOLFCSLDLFSCILCVLYRIIDEE	1006
Dd	954	dyyagasygrckrlgllslsdqvlsqjinprkctfgqlfcgsldnfgllcvglyrmiddee	1013
Oy	1009	LNPENKRFPVTRPANEFKLRLSPLVCARIPESACK	1045
Dd	1014	psgehkrvtlrpsnechllipsdlvtcalpfnltcgk	1050
 RESULT 4 AAI32017 ID AAI32017 standard; Protein; 1196 AA. XX AC AAI32017; XX DT 05-JAN-2000 (first entry) DE Mouse cation channel protein. XX KW Cation channel protein; CCP; ion transport; arrhythmia; KM diabetes mellitus; seizure; asthma; hypertension; therapy; XX protein engineering; mouse. OS Mus musculus. XX FH Key Location/Qualifiers FT Region 61..119 FT /note="Crystal region" XX PN WO9947923-A2. XX PD 23-SEP-1999. XX PE 22-MAR-1999; 99MO-USO6307. XX PR 20-MAR-1998; 98US-0045529. PR 02-APR-1998; 98US-0054347. XX PA (UYRQ) UNIV ROCKEFELLER. XX PI Mackinnon R; XX DR WPI: 1999-601131/51. XX PT Assays for screening compounds which interact with cation channel - PT proteins, useful for providing agents for treatment of diseases - XX XX Claim 21; Page 144-147; 165pp; English.			

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2001, 09:43:27 ; Search time 9921.66 Seconds
(without alignments)
3162.175 Million cell updates/sec

Title: US-09-176-664-17
Perfect score: 3319
Sequence: 1 atgttcagactaagctacg.....tcttctcctaagcaaatag 3319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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258: gb_est189:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	311	9.4	604	142	BE981888	BE981888 UI-M-CGDP
2	233.2	7.0	524	162	BE012861	BE012861 122576 MA
3	227.4	6.9	652	229	AO477745	AO477745 CITR1-EL1
4	219	6.6	329	189	T71508	T71508 yd35h12.r1
5	215.6	6.5	745	111	AW052067	AW052067 wx25g11.x
6	187	5.6	425	189	T83073	T83073 yd40d04.r1
7	183.2	5.5	720	22	A1633673	A1633673 tnl1b08.x
8	175.6	5.3	509	16	AA488159	AA488159 UI-M-BH3-
9	165	5.0	449	244	AZ491148	AZ491148 1M0324J05
10	153.6	4.6	509	16	A1129381	A1129381 qc34d02.x
11	149.2	4.5	507	16	A1095675	A1095675 qb20a12.x
12	147.8	4.5	493	16	A1147610	A1147610 qb22a02.x
13	138.4	4.2	493	18	A1276627	A1276627 q164b06.x
14	136.4	4.1	504	23	A1670742	A1670742 wc28f10.x
15	128.2	3.9	377	2	AA072586	AA072586 mm73b05.r
16	126.4	3.8	453	19	A1335943	A1335943 q137g04.x
17	123	3.7	479	19	A1373399	A1373399 q289f05.x
18	122	3.7	395	10	AA644503	AA644503 a173b06.r
19	114.4	3.4	417	16	A1091147	A1091147 q946f12.s
20	101	3.0	582	16	A1105495	A1105495 SNMCMC22
21	100.4	3.0	395	19	A1342342	A1342342 q272a12.x
22	97.6	2.9	1061	220	CNS01YE	AL173507 Tetrarodon
23	96	2.9	447	14	A1005321	A1005321 ou13h03.x
24	90.4	2.7	345	116	AA492014	AA492014 UI-M-BH3-
25	90.4	2.7	414	187	R15380	R15380 yf30f04.r1
26	89.8	2.7	648	241	AZ332812	AZ332812 1M061P20
27	89	2.7	531	251	AZ904065	AZ904065 RPTC1-24-2
28	89	2.7	652	248	AZ744416	AZ744416 RPTC1-24-1
29	88.8	2.7	626	236	AZ003347	AZ003347 RPTC1-23-3
30	87.2	2.6	360	155	C62155	C62155 C62155 yu11
31	84.6	2.5	730	108	AU171675	AU171675 AU171675
32	84.2	2.5	415	3	AA194929	AA194929 zrl3h11.r
33	84.2	2.5	423	104	A1962224	A1962224 wq4b002.x
34	84.2	2.5	477	136	BE502286	BE502286 hy15d09.x
35	82	2.5	468	139	BE765223	BE765223 il2-MT010
36	81.4	2.5	293	152	BC347800	BC347800 dac80b10.
37	80.6	2.4	981	221	CNS04EXX	AL287142 Tetrarodon
38	79.4	2.4	309	3	AA194930	AA194930 zrl3h11.s
39	79	2.4	419	13	AA906575	AA906575 ol22c02.s
40	77.2	2.3	811	220	CNS030Y2	AL222851 Tetrarodon
41	77	2.3	480	11	AA758685	AA758685 an75b11.s
42	76.8	2.3	358	15	A1080449	A1080449 ox82e08.s
43	76.2	2.3	633	19	A1402739	A1402739 GH22026.5
44	76	2.3	405	189	T71346	T71346 yd35h12.s1
45	74	2.2	331	111	AW080780	AW080780 xc52a12.x

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	BE981888	UI-M-CGDP-bde-d-09-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone	BE981888	BE981888	GI:10651471	house mouse, Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 604)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)

MEDLINE COMMENT

97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the retina tissue cDNA library preparation: M.B. Soares Lab Clone distribution. Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA=yes.

FEATURES

source
1..604
/location="Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CGDP-bde-d-09-0-UI"
/clone_1lb="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.
TAG_LIB=NIH_BMAP_Ret4_S2
TAG_TISSUE=adult-retina
TAG_SEQ=GTCCAGCGCCGAC"

BASE COUNT 161 a 153 c 131 g 159 t

ORIGIN

Query Match 9.4%; Score 311; DB 142; Length 604;
Best Local Similarity 70.8%; Pred. No. 2.1e-77;
Matches 413; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
QY 2255 tgcattcgggtctctgacctatctacagagaagatgagatctctccggaatttccc 2314
DB 4 TTTTGGGCTCTGGAGTACTCCAGAGATGGCATTTCTCCGAACCTTCCCA 63
QY 2315 agatatcattcctcctgagatgacttattctgagacctcattcgcgcacaatag 2374
DB 64 AGATACACATTATGCTGATCTGCATCTGATGAGATCTGATGATGATGATGATG 123
QY 2375 agcaatgctcattgctgctgctgctgctgctgctgctgctgctgctgctgctg 2434
DB 124 AGCAGTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
QY 2435 tggtagacacagac 2494
DB 184 TGGTGACACAGAGACACATGATGATGATGATGATGATGATGATGATGATGATG 243
QY 2495 cctcgcacccgtaaccctcgaagtgtcagagagagacccaggttaccacaatgacata 2554
DB 244 CTACTCCAGAGCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 303
QY 2555 agaatacaactgcgcgaagaatccctacacacacacacacacacacacacacac 2614
DB 304 GGAACCAAGATACAAAGATCCCATTTTCATGAACTGAAGAAATCCCTCAACATCC 363
QY 2615 acctattgacacgcttggtagactggaagggtccctccaagaacaaattgacttca 2674

Db 364 ACTTTATGACAGATGGGGGACATGGAATGCTCAAGGACATACCTTGACATCTCA 423
Qy 2675 gcaatgaccttcttaacggagacgtttcttccagcaagctcttgatctctgctgcca 2734
Db 424 GCACCTCTTCTCCACCGGAGCTGTCTTTTCAGACACCTTCTTGATTTCTCTCGGCCA 483
Qy 2735 cggcctcttcaattatcaatgctcctggaattgcttcaagatgctgctgagagagaa 2794
Db 484 CGTCTTCTTCAATTAACAGATGCTGGAATTAAGTCTGAGATGAGTCAAGGAGCATAA 543
Qy 2795 gtctcagcagacaacatttagataaagctatg 2837
Db 544 GCCTGAGATGAGACACTATTGTGTTAAGAGAGAACCCCTTAG 586

RESULT 2
LOCUS BE012861 524 bp mRNA EST 09-JUL-2000
DEFINITION 122576 MARC 1pIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE012861
VERSION BE012861.1 GI:8273800
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM pig.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (bases 1 to 524)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grose, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTCACAGTACAGCAGC
Place: 46 row: B column: 16
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source location/Qualifiers

1..524
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1pIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

BASE COUNT 132 a 119 c 134 g 139 t
ORIGIN

Query Match 7.0%; Score 233.2; DB 162; Length 524;
Best Local Similarity 80.1%; Pred. No. 3.4e-55;
Matches 301; Conservative 0; Mismatches 68; Indels 7; Gaps 2;

Qy 1977 aagcacttgagagatcaaacctccaccagagctcttcaacagatgtagaacaaga 2036
Db 155 ACACACTGTGCTTACATGTCACAGACATTCAGCGCTTTCACTATGAATGGAACAA-- 212

Qy 2037 ttctgacagcttgatagagatggttctacgtgtgcaaaccaacctcttgacaa 2096
Db 213 ----GACCACTTGATTAACACTGGCATGTTTCTGCTGTCAGAGCCACCCCATTTGACAA 268

Qy 2097 ggtgactctgaaacgaactggaagtcagaagtaagttcggaaacataatgtagcatg 2156
Db 269 AATGATTTCTGAAGAAAGAACTGACAAAGTCAAAACATGATTTCCGAAACCATCTGCATG 328
Qy 2157 tggatctt-ggaagatgcccactcagcccgatggggtcttggaactttgtaatgcccttga 2215
Db 329 TGTCTTGGAGATGCCCATTCACACCTGATGGGGCTTCGGAATTTGTAAATCCACTGA 388
Qy 2216 gaagcagacactatcacgaagaagagctgaagacatagttcatatggctcctgagac 2275
Db 389 GAGCTAGCACTACACCCGCAAGAGCTGAAGACATTTGTTGGGTCTCTGGATT 448
Qy 2276 atctacagaagaatggagatcttctccgaatttcccagatatacatctgctgagac 2335
Db 449 ACCTGACAGAGATGGCGATTCCTCGGAATTTCCCGAGATATACTTCTGCTGGAT 508
Qy 2336 gtgacttattctg 2351
Db 509 CTGCGCTTATTCTGG 524

RESULT 3
LOCUS A0477745 652 bp DNA GSS 23-APR-1998
DEFINITION CITR1-EI-2591F7.TF CITR1-EI Homo sapiens genomic clone 2591F7, DNA
sequence.
ACCESSION A0477745
VERSION A0477745.1 GI:4659864
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 652)

REFERENCE Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building

JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

Email: hbeet@igf.org
Clones are available from Research Genetics (Info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source location/Qualifiers

1..652
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2591F7"
/clone_lib="CITR1-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 198 a 165 c 122 g 167 t
ORIGIN

Query Match 6.9%; Score 227.4; DB 229; Length 652;
Best Local Similarity 98.8%; Pred. No. 1.7e-53;
Matches 250; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 3041 aagagtttgcaccgagccagcaatgaattcaagctgctgcttgaatctgctgt 3100
Db 402 ACAAGTTTGATCACCCGCGACCAATGATTAAGTGTGCTTCAAGATCTTGCTG 461

	BASE COUNT	98 a	60 c	71 g	95 t	5 others
	ORIGIN					

OY	3101	cttgccacatccccctcgcgaactgcttctctaaaggaalgaagaagtcttcattggcaaa	3160
Db	462	TTTGCGCATACCCCTTCAGCAGCACTGCTTCTTTATTAAGAATGAACAAGTTTCATTGGCAA	521
OY	3161	agtcatacgaaaatctgtlaataaagcatcacagacaagaacagagacatctcagacaant	3220
Db	522	AGTCATATGAATAATGTAAATTAAGCATGCATCACAGCAACAGA--GACACATTTCAACACCAAT	580
OY	3221	tgtctctcccaccatcttgatctgaagttacgcgagacatctgtatctacacagctctctacca	3280
Db	581	TGTCTCTCCCA-CCAATGATTTTCAGTTACTGACAGACATTTGATTCACCACAGTCTATTTCACA	639
OY	3281	gccgagagaactaac	3293
Db	640	GCCGAGAGCACTAAC	652

RESULT	4					
LOCUS	T71508	329 bp	mRNA	EST	15-MAR-1995	
DEFINITION	yds3hl2.r1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone					
ACCESSION	IMAGE:110279	5', mRNA sequence.				
VERSION	T71508					
KEYWORDS	T71508.1	GI:686029				
SOURCE	EST.					
ORGANISM	human.					
REFERENCE	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 329) Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman, 'M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Mairra,M., Parsons,J., Ritkin,I., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterson, 'R., Williamson,A., Wohlmann,P. and Wilson,R. The Washu-Merck EST Project Unpublished (1995) Other ESTs: yds3hl2.s1 Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 180 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNLN ; contact the IMAGE Consortium (info@image.lnl.n.gov) for further information. Seq primer: M13RP1 High quality sequence stop: 180. Location/Qualifiers 1..329 /organism="Homo sapiens" /db_xref="GDB:465896" /db_xref="taxon:9606" /clone_image="IMAGE:110279" /clone_lib="Soares fetal liver spleen INFLS" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /note="Organ: Liver and Spleen. Vector: pT773D (Pharmacia) with a modified polylinker. Site_1: Pac I; Site_2: Eco RI 1st strand cDNA was primed with a Pac I - oligo(dT) primer '5' AACGCGAAGATTAATTAAGATCTTTTTTTTTTTTTTTTTTTT 3'', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Boinado."					

TITLE	JOURNAL	COMMENT
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	Best Local Similarity	95.1%	Pred. No. 3.4e-51.	
	Matches 234.	Conservative 0.	Mismatches 10.	Indels 2.
				Gaps 1.
QY	2734	acggcctctcaaatatcatcgtccctggaatgcttcagatgctcggcgacaagagagta	2793	
Db	84	AAGCCTTCATCATTTATCATCATGCTCGGAATTTGCTTCAGAGACTGGTGACACAGNGAGTA	143	
QY	2794	agctctcaagcgggaacaaactttagataagataaagctatagtggtgacagatgctgc	2853	
Db	144	AGTTCTACGCTGGAAACAACATTTAGATTAAGGATTAAGTCTATGGTGTGNCACATTAAGCTTC	203	
QY	2854	acgcgcctctgctctgcaagaacacgcgctgtaagctcgggctctctgctccctacacgaaac	2913	
Db	204	ACGTCGCTCTTGCTCGGAAGAACCCNGTGAAGCTGGGGCTTCTCTCTTACACGAAC	263	
QY	2914	atttlatcagaagctbtaatccaaagaacaccccttggacaactgct--ctggtgcctaatg	2971	
Db	264	ATTATTACAGACGTTAAACCNAGAAACACCTTNGACAACTGTTCTGTGGCCTCATTAAG	323	
QY	2972	atctctt 2977		
Db	324	GTCCTT 329		

FEATURES	source	1. .745	Location/Qualifiers
AM052067/c	LOCUS	AM052067 745 bp mRNA	EST 09-MAR-2000
AM052067/c	DEFINITION	w225911.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:254740 3'	
AM052067	ACCESSION	Similar to TR:Q28204 Q28204 LARGE CONDUCTANCE CALCIUM-ACTIVATED	
AM052067	POTASSIUM CHANNEL ALPHA SUBUNIT ;	mRNA sequence.	
AM052067.1	GI:5914426		
EST.			
human.			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
1 (bases 1 to 745)			
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
Tumor Gene Index			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgaps-rt@mail.nih.gov			
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.			
Emmert-Buck, M.D., Ph.D.			
CDNA Library Preparation: M. Bento Soares, Ph.D.			
CDNA Library Arrayed by: Greg Lennon, Ph.D.			
DNA Sequencing by: Washington University Genome Sequencing Center			
clone distribution Information can be			
found through the I.M.A.G.E. Consortium/MLN1 at:			
www-bio.llnl.gov/dbfp/image/image.html			
Insert length: 927			
Std Error: 0.00			
Seq primer: -40UP from Gibco			
High quality sequence stop: 450.			

Query Match

6.68; Score 219; DB 189; Length 329;

BASE COUNT

181 a	162 c	176 g	226 t
-------	-------	-------	-------

LOCUS AI129381/c
DEFINITION qc34dd02.x1 Soares_pregnant_uterus_NbHpu Homo sapiens cDNA clone IMAGE:1711491 3' similar to YR:Q12791 Q12791 CALCITRIUM-ACTIVATED POTASSIUM CHANNEL ; contains Alu repetitive element; mRNA sequence
ACCESSION AI129381
VERSION AI129381
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 509)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: ccgabs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 699 std error: 0.00
Seq primer: -40m13 fwd. ER from Amersham
High quality sequence stop: 444.
Location/Qualifiers
1..509

	FEATURES	SOURCE
	Location/Qualifiers	
1..509	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:1711491"	
	/clone_1lb="Soares_pregnant_uterus_Nbhpu"	
	/sex="female"	
	/dev_stage="adult"	
	/lab_host="DH10B"	
	/note="Organ: uterus; Vector: pT73-Pac; Site:1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - alcgga(gat) primer [5', AATCGAAGAATTTCGCGGCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."	
BASE COUNT		
ORIGIN	131 a	108 c 118 g 152 t

Query Match	4.6%	Score 153.6	DB 16	Length 509
Best Local Similarity	58.5%	Pred. No. 1.9e-32		
Matches 289	Conservative 0	Mismatches 199	Indels 6	Gaps 1
QY 1333	atccatatacagatactgcataatccataatacaaggttatlctctccaaagatattccacgtctgg	1392		
Db 509	ATCATCACTCAAAATGCTGACGATATCAACAACAGGCCCATCTGCTTAACATCCCGAGCTGG	450		
QY 1393	aactggacacccggagacacatcatctgcttctgcttgaatataaacctggattatcgcg	1452		
Db 449	AATTGGAAAGAAAGCGATGATGACCGCATCTGCGCCGACAGATTGAAGTTGGGCTTCATAGCC	390		
QY 1453	caaggctcttggctggccaggctctgtgtacccctccaaactctctatctgttgagcaaaac	1512		
Db 389	CAGACCTGCTGCTGGCTCAAAAGGCTCTTCCACACATGCTTGGCCAACTCTTTCCATGAGGTCA	330		
QY 1513	aaaaaggtatgcctcaaaacagacctcggaagaacaccttcttgaatagcatgaataaaca	1572		
Db 329	TTTCATTAAGGATTTGAGGAAGACACATGGGCGAGAAATACCTTGTGGAAGGAGTCCAAATGA	270		
QY 1573	attctgacccaacgctctctctgtagtacttctgctgaatgaagcttctctgaagtgcgcg	1632		
Db 269	ATGTACACAGAATATCTCTCCAGTCCCTTCGCGGGCTGTGCTCTCCCTACTTTGTGAG	210		
QY 1633	ctctgcttcttgaagaatgaactcctctgttctgaagcatatcgaaatacaagctcctctttag	1692		
Db 209	CTGTCTTTTGTGTAACCTCAAGCTCTCAATGATGAGCATTTGAGTAACAAAGTC-----TGCC	156		

OY	1693	gaiggttctcgtgctgcataactaaatccaccctccaaagtaggaatacgtlaagaaccca	1752
Db	155	AACCGAGAGAGCCGTATATTAACTTGGAACCACTTAAATCATCCAGAAAGTACT	96
OY	1753	ttaggtctcttaattcctgaacctccaagaagcgtcagaagaagccttgtttactgttca	1812
Db	95	TTTAGATTTTTCATCGGAAGCTATGCCAAGAAGATTAAAGGGCATTTTTTACTGCAAG	36
OY	1813	gtctgtcatgatga	1826
Db	35	GCTGTGTCATGATGA	22

RESULT	11
AI095675/c	
LOCUS	AI095675
DEFINITION	507 bp mRNA
	EST
	05-OCT-1998
	gb20a12.x1 Soares_pregnant_uterus_NbHpu Homo sapiens cDNA clone
	IMAGE:1696798.3 similar to TR:012791 Q12791 CALCIUM-ACTIVATED
	POTASSIUM CHANNEL ;, mRNA sequence.
ACCESSION	AI095675
VERSION	AI095675.1
KEYWORDS	GI:3434651
SOURCE	EST.
ORGANISM	human.
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 507)	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap .	Unpublished (1997)	
	National Cancer Institute,	Cancer Genome Anatomy Project (CGAP),	Tumor Gene Index	
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov .			
	This clone is available royalty-free through LBNL; contact the			
	IMAGE Consortium (infoimage.lbl.gov) for further information.			
	Insert Length: 664	Std Error: 0.00		
	Seq primer: -40m3 fwd. ET from Amersham			
	High quality sequence stop: 394.			
	Location/Qualifiers.			
	1..507			

FEATURES	source
location/Qualifiers	1..507
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:1636798"	
/clone_lib="Scares_pregnant_uterus_Nbhpu"	
/sex="female"	
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/lab_host="DH10B"	
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BASE COUNT	133 a 109 c 116 g 148 t 1 others
ORIGIN	

	Query Match	4.5%	Score 149.2;	DB 16;	Length 507;
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Db	504	AGAAATCATCTACTCAATGCTGTCAGATATACAAANAAAGGCCCATCTCTTAACATCCCGAAC	445		
Qy	1390	tggaaacttggagacacggagacacacatcatcttcttgcgtgaaattaaacttggattttac	1449		
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[illegible]

ORIGIN

Query Match	4.58;	Score 147.8;	DB 16;	Length 493;
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Matches 282; Conservative	0;	Mismatches 197;	Indels 6;	Gaps 1.

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Db	493	CAATAGCTGCAGATATCCAAACAAGAGCCCATCTGCTCTAAACATCCGACATGGAATTTGGAAA	434
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LOCUS	AI276627/c		
DEFINITION	g164506.x1 Soares.NHMP-1SI Homo sapiens cDNA clone IMAGE:1877075		
	3, similar to TR:012791 Q12791 CALCIUM-ACTIVATED POTASSIUM CHANNEL		
	; mRNA sequence.		
ACCESSION	AI276627		
VERSION	AI276627.1	GI:3898901	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1. (bases 1 to 493)		
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgp .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgaaps-r@mail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2001, 09:50:45 ; Search time 244.36 Seconds
(without alignments)
2571.303 Million cell updates/sec

Title: US-09-176-664-17

Perfect score: 3319
Sequence: 1 agtttcagactaagctagc.....tcttctcgaagaatag 3319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	36.6	1.1	7218	1 US-08-232-463-14	Sequence 14, Appli
4	35.4	1.1	2876	4 US-09-134-607A-9	Sequence 9, Appli
5	35.4	1.1	2876	4 US-09-134-607A-14	Sequence 14, Appli
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7	33.6	1.0	1518	2 US-08-929-501-4	Sequence 4, Appli
8	33.6	1.0	1518	2 US-08-929-501-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1
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Sequence 6, Application US/09035648
Patent No. 6100031
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
TITLE OF INVENTION: GROWTH AND PROLIFERATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035, 648
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/818, 829
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Melkijohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-035-648-6

Query Match 1.7%, Score 57.4, DB 3, Length 311;
Best Local Similarity 59.5%, Pred. No. 4.3e-08;
Matches 97, Conservative 0, Mismatches 66, Indels 0, Gaps 0;

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6      ; GENERAL INFORMATION:
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8      ; TITLE OF INVENTION: POLYNUCLEOTIDES CONTROLLING THE EXPRESSION
9      ; TITLE OF INVENTION: OF AND CODING FOR GENE B IN TOMATO AND USE
10     ; TITLE OF INVENTION: OF SAME FOR ALTERING CAROTENOID
11     ; TITLE OF INVENTION: BIOSYNTHESIS
12     ; NUMBER OF SEQUENCES: 25
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: Mark M. Friedmann c/o Anthony Castorina
15     ; STREET: 20001 Jefferson Davis Highway, Suite 207
16     ; CITY: Arlington
17     ; STATE: Virginia
18     ; COUNTRY: United States of America
19     ; ZIP: 22202
20     ;
21     ; COMPUTER READABLE FORM:
22     ; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
23     ; COMPUTER: twinhead, Slimnote 890TX
24     ; OPERATING SYSTEM: MS DOS version 6.2,
25     ; OPERATING SYSTEM: Windows version 3.11
26     ; SOFTWARE: Word for Windows version 2.0,
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28     ; APPLICATION NUMBER: US/09/134,607A
29     ; FILING DATE:
30     ; CLASSIFICATION: 800
31     ; PRIOR APPLICATION DATA:
32     ; APPLICATION NUMBER:
33     ; FILING DATE:
34     ; ATTORNEY/AGENT INFORMATION:
35     ; NAME: Friedmann, Mark M.
36     ; REGISTRATION NUMBER: 33,883
37     ; REFERENCE/DOCKET NUMBER: 325/12
38     ; TELECOMMUNICATION INFORMATION:
39     ; TELEPHONE: 972-3-562553
40     ; TELEFAX: 972-3-562554
41     ; TELEX:
42     ; INFORMATION FOR SEQ ID NO: 14:
43     ; SEQUENCE CHARACTERISTICS:
44     ; LENGTH: 2876
45     ; TYPE: nucleic acid
46     ; STRANDEDNESS: double
47     ; TOPOLOGY: linear
48     ;
49     ; US-09-134-607A-14

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[illegible]


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ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,501
FILING DATE: 15-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1753 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-929-501-3

Query Match          1.0%; Score 33.6; DB 2; Length 1753;
Best Local Similarity 52.1%; Pred. No. 3.8;
Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

OY 2776 ctgctgcacaggaagaagttaagttcctaagtcgtgaacaacaattagataagaataaagttcat 2835
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Db 655 CTGTTGACCCCAAGGTGGTTCATCTTCATCTGCAGAGATCAATGGAGTAAGAATGCCCTCGTA 596

OY 2836 ggtgttgcaagatlaactgcagctgcctcttgccttgaaagaaccgggttaagcttgggctt 2895
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Db 595 AGTCACAGTAAAAAAGAAATAAGATCTTAATTGAACCTTGCGATTCGACGGGGCACACTG 536

OY 2896 ctgccttacacgaaccttta 2919
    ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 535 CTTTCATAAATTCAACCGCAGATTA 512

RESULT 15
US-09-140-177-1
: Sequence 1, Application US/09140177
: Patent No. 6042825
: GENERAL INFORMATION:
: APPLICANT: Ramaswamy Chandrashekar
: APPLICANT: Naotoshi Tsuji,
: TITLE OF INVENTION: PARASITIC HELMINTH ASPARAGINASE
: TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
: TITLE OF INVENTION: USES THEREOF
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carol Talkington Verser, Ph.D.
: ADDRESSEE: Heska Corporation
: STREET: 1825 Sharp Point Drive
: CITY: Fort Collins
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80525
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: Windows 95
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2001, 19:18:11 ; Search time 733.38 Seconds
(without alignments)
2841.645 Million cell updates/sec

Title: US-09-176-664-17

Perfect score: 3319
Sequence: 1 atgttcagactacagctacg.....tctttcctaagcaatag 3319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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22: /cgnl_9/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	3318.6	100.0	3319	AAK55524
2	3163.6	95.3	3247	AAK55525
3	1857	56.0	3339	AAK55514
4	376	11.3	416	AAK55515
C 5	94.4	2.8	936	AAK58252
C 6	94.4	2.8	936	AAK58254
C 7	94.4	2.8	936	AAK58257
C 8	94.4	2.8	936	AAK58259
C 9	94.4	2.8	936	AAK58262
C 10	94.4	2.8	938	AAK58255
C 11	93.4	2.8	936	AAK58252

12	93.4	2.8	936	22	AAK58254	Oligonucleotide D1
13	93.4	2.8	936	22	AAK58257	Oligonucleotide D1
14	93.4	2.8	936	22	AAK58259	Oligonucleotide D2
15	93.4	2.8	936	22	AAK58262	Oligonucleotide D2
16	93.4	2.8	938	22	AAK58255	Oligonucleotide D1
17	57.4	1.7	311	18	AAK91705	Gene 056 fragment
18	41.6	1.3	244	22	AAK58238	Oligonucleotide D1
19	41.6	1.3	1887	20	AAK13115	Enterococcus faecae
20	41	1.2	244	22	AAK58238	Oligonucleotide D1
21	40	1.2	580073	18	AAK58840	Mycoplasma genital
22	38.4	1.2	1866	20	AAK59653	Nucleic acid sequen
23	37.4	1.1	6531	20	AAK13012	Enterococcus faeca
24	36.8	1.1	1449	18	AAK72643	Human calpastatin
25	36.6	1.1	1549	21	AAK16638	Human secreted pro
26	36.6	1.1	2919	21	AAK38526	CDNA encoding Euca
27	36	1.1	49998	20	AAK33518	Human kidney amino
28	35.6	1.1	2701	20	AAK6143	DNA encoding a pot
29	35.4	1.1	2876	20	AAK251517	L. esculentum lycco
30	35.4	1.1	16941	21	AAK234737	Drosophila disaeti
31	35	1.1	9828	19	AAK52174	Streptococcus pneu
32	34.6	1.0	1331	21	AAK233370	Human secreted pro
33	34.4	1.0	767	20	AAK16218	Human gene express
34	34.4	1.0	1206	17	AAK09352	Aureobasidin resis
35	34.2	1.0	1995	19	AAK53550	DNA encoding a ace
36	34.2	1.0	3451	18	AAV02308	Cell membrane prot
37	34.2	1.0	7481	18	AAV4547	Staphylococcus aur
38	34.2	1.0	9326	21	AAK51236	Staphylococcus aur
39	34.2	1.0	17310	18	AAK74334	Staphylococcus aur
40	34	1.0	300	20	AAK12908	Human gene express
41	34	1.0	789	20	AAK15761	Human gene express
42	34	1.0	789	20	AAK15762	Human gene express
43	33.8	1.0	1306	22	AAK1092	Soybean geranylger
44	33.8	1.0	1401	21	AAK00086	Human zslg99 degen
45	33.8	1.0	1729	10	AAK91686	Sequence of Saccha

ALIGNMENTS

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ID AAK55524	standard; DNA: 3319 BP.
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AC	
XX	
DT 26-JUL-1999	(first entry)
XX	
DE	
XX	
XX	
KW	Nucleotide sequence of hsl03-1.
KW	Voltage-gated, pH sensitive; potassium channel; S103; spermatocyte;
KW	sperm capacitation; acrosome reaction; fertilization; infertility;
KW	contraceptive; sperm physiology; channel protein; gene therapy; ss.
XX	
OS	Homo sapiens.
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PN	W09920754-A1.
XX	
PD	29-APR-1999.
XX	
PF	21-OCT-1998; 98WO-US22321.
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PR	27-FEB-1998; 98US-0076172.
XX	
PR	22-OCT-1997; 97US-0063138.
XX	
PA	(UNIW) UNIV WASHINGTON.
XX	
PI	Salkoff L, Schreiber M, Silvia C;
XX	
XX	WPI: 1999-326593/27.
DR	P-FSDB: AAK1442.
XX	
PT	Voltage-gated, pH-sensitive potassium channel useful in gene therapy

PS Claim 9: Page 79-80; 93pp: English.
XX The invention relates to a voltage-gated, pH sensitive potassium channel
CC SLO3, expressed in spermatoocytes. SLO3 has, as a monomer, calculated
CC molecular weight 120-156 kD; has unit conductance (as a functional
CC tetramer, when expressed in Xenopus oocytes) of 80-120 pS; has increased
CC activity at intracellular pH above about 7.1 and binds specifically to
CC polyclonal antibodies against sequences shown in AY13437, AY13438,
CC AY13442, and AY13443. SLO3 is involved in sperm capacitation and/or the
CC acrosome reaction, essential steps in fertilization. SLO3, and the
CC nucleic acid encoding it, are used to identify specific inhibitors and
CC activators (potentially useful for treating infertility and as
CC contraceptives), also for studying sperm physiology in vitro.
CC SLO3-specific antibodies are used for diagnostic detection of SLO3
CC expression. SLO3, as part of a chimera with another channel protein, can
CC be used as a reporter for measuring changes in potassium concentration,
CC current flow, ion flux, etc. Fragments of SLO3 nucleic acid are useful as
CC probes for identifying homologs, variants and mutants associated with
CC disease; to detect SLO3-related mRNA or protein; for chromosomal
CC localization; in gene therapy; for identifying potential modulators; to
CC measure up-regulation of SLO3 in drug screening assays and for production
CC of recombinant SLO3 protein. The present sequence represents the
CC nucleotide sequence of hSLO3-1.
XX
XX
S0 Sequence 3319 BP; 927 A; 758 C; 697 G; 936 T; 1 other;

Query Match 100.0%; Score 3318.6; DB 20; Length 3319;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 acgagatcaagaacagatcatctctctctcttctgtgacctcttcagttgacatc 120
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QY 121 atccgtgtgacttcagctgacgtacgtgagatcctgttaaaaaatgacatcaagga 180
DB 121 atccgtgtgacttcagctgacgtacgtgagatcctgttaaaaaatgacatcaagga 180
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RESULT 2
AAX55525
ID AAX55525 standard; DNA: 3247 BP.
AAX55525;
26-JUL-1999 (first entry).
DE Nucleotide sequence of hsl03-2.
XX
AC
AC AAX55525;
DT 26-JUL-1999 (first entry).
XX
DE Nucleotide sequence of hsl03-2.
XX
KW Voltage-gated; pH sensitive; potassium channel; sl03; spermatocyte;
KW sperm capacitation; acrosome reaction; fertilization; infertility;
KW contraceptive; sperm physiology; channel protein; gene therapy; ss.
OS Homo sapiens.
XX
PN W09920754-A1.
XX
PD 29-APR-1999.
XX
PF 21-OCT-1998; 98WO-US22321.
XX
PR 27-FEB-1998; 98US-0076172.
PR 22-OCT-1997; 97US-0063138.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Salikoff L, Schreiber M, Silvia C;
XX
XX WPI: 1999-326593/27.
DR P-PSDB; AAY13443.
XX
XX Voltage-gated, pH-sensitive potassium channel useful in gene therapy
PT
XX
PS Claim 9; Page 81-82; 93pp; English.
XX

Db 1669 cgtlaagaaacactlaagggttcttatttgctgaaactccaagaagctgaagaagccttg 1728
Oy 1801 ttttactcttcaagctctgtcaatgatagtgtgttcattctctgaagctaatcaaacctgtgac 1860
Db 1729 ttttctcttctcagctctgtcatatgatatgtgttcattctcgaagctaatcaaacctgtgac 1788
Oy 1861 tgcanaaagcagaagccggaagcagacataccaaagctcagatgaagaagataaataatgt 1920
Db 1789 tgcanaaagcagaagccggaagcagacataccaaagctcagatgaagaagataaataatgt 1848
Oy 1921 ctgaagggaatctctctctgtataltacaggcgagga tttctcgcgaagggtatctgcaagc 1980
Db 1849 ctgaagggaatctctctctgtataltacaggcgagga tttctcgcgaagggtatctgcaagc 1908
Oy 1981 actctgagacataatcaaaactccaacaggaactctcaacatgatagttagaacaagatctc 2040
Db 1909 actctgagacataatcaaaactccaacaggaactctcaacatgatagttagaacaagatctc 1968
Oy 2041 gaccagcttgatagcagtgagatgtttcacctgtgcaaaccaacctcttggaacaagctg 2100
Db 1969 gaccagcttgatagcagtgagatgtttcacctgtgcaaaccaacctcttggaacaagctg 2028
Oy 2101 actctgaaacggaactctgcaagtcgaagataaagtttcggaaccacatactgtagcatgtgta 2160
Db 2029 actctgaaacggaactctgcaagtcgaagataaagtttcggaaccacatactgtagcatgtgta 2088
Oy 2161 ttgtgagatgccaactcagccccgattggggtctcggaactctgttaattgcctctgagacc 2220
Db 2089 ttgtgagatgccaactcagccccgattggggtctcggaactctgttaattgcctctgagacc 2148
Oy 2221 agcaactataccagaagaagctggaagacataagtcattcaggtgtctctggaacatacta 2280
Db 2149 agcaactataccagaagaagctggaagacataagtcattcaggtgtctctggaacatacta 2208
Oy 2281 cagagaagaatgagcgaattctccggaatttcccgagataatacatctgcctgagatgtgca 2340
Db 2209 cagagaagaatgagcgaattctccggaatttcccgagataatacatctgcctgagatgtgca 2268
Oy 2341 cttaattctgagagactccatctgctcgccgaacataagacaaatgtctcatgtgtctcttg 2400
Db 2269 cttaattctgagagactccatctgctcgccgaacataagacaaatgtctcatgtgtctcttg 2328
Oy 2401 tcccccccaaccccaacatcaagcaaacaggaactctgtgtagacaagaaacacatactgca 2460
Db 2329 tcccccccaaccccaacatcaagcaaacaggaactctgtgtagacaagaaacacatactgca 2388
Oy 2461 accctacacatctggaatccttgcaaatgtgacatccctctgaccgctcacctcagtgta 2520
Db 2389 accctacacatctggaatccttgcaaatgtgacatccctctgaccgctcacctcagtgta 2448
Oy 2521 gagagagatcccggttaacaaatgagacataatgagaatacaactgcccgaagaatccct 2580
Db 2449 gagagagatcccggttaacaaatgagacataatgagaatacaactgcccgaagaatccct 2508
Oy 2581 atccctactgaaactgaaaaatccctcccaacatctcattatgaaacagcttggtgagactg 2640
Db 2509 atccctactgaaactgaaaaatccctcccaacatctcattatgaaacagcttggtgagactg 2568
Oy 2641 gaagggtccctccaaagaacaaatctgcaatctcagcaactgaccttctctacgggcaactgt 2700
Db 2569 gaagggtccctccaaagaacaaatctgcaatctcagcaactgaccttctctacgggcaactgt 2628
Oy 2701 ttttccagaagcttttgatattctctgtctgcccgaagcgcctttaaataattatgtcccg 2760
Db 2629 ttttccagaagcttttgatattctctgtctgcccgaagcgcctttaaataattatgtcccg 2688
Oy 2761 gaattgtctcagaatgctgtgtagacaggaagataagttctcagctggaacaacattagat 2820
Db 2689 gaattgtctcagaatgctgtgtagacaggaagataagttctcagctggaacaacattagat 2748
Oy 2821 aagataaagctatagtgtgtgtagatagctgacagctgcctctgtctggaagaacccg 2880

Db 2749 aagataaagctatagtgtgtgtagatagctgacgctgcctctgtctggaagaacccg 2808
Oy 2881 tgaagctgggggtctctgtctcttaacagaacacatttatacgaagcttaataccaagaaac 2940
Db 2809 tgaagctgggggtctctgtctcttaacagaacacatttatacgaagcttaataccaagaaac 2868
Oy 2941 acccttgacaactgtctcgtgctcaatagaaccttttggatccotgtgtgtgctta 3000
Db 2869 acccttgacaactgtctcgtgctcaatagaaccttttggatccotgtgtgtgctta 2928
Oy 3001 taccgaataatgatagaagaagagctcaacccagaanaaaggattgtgatacccg 3060
Db 2929 taccgaataatgatagaagaagagctcaacccagaanaaaggattgtgatacccg 2988
Oy 3061 ccagccaatgaaatcaagctgtgccttcaagatctgtgttttggccaataccctcagc 3120
Db 2989 ccagccaatgaaatcaagctgtgccttcaagatctgtgttttggccaataccctcagc 3048
Oy 3121 actgctgttataaagaagataagagctctcatctgcaaaagctcatatgataatgtlaac 3180
Db 3049 actgctgttataaagaagataagagctctcatctgcaaaagctcatatgataatgtlaac 3108
Oy 3181 aagaatcacagaacaagagagacacatctcagaacaacaaatgttccctccacacatgtat 3240
Db 3109 aagaatcacagaacaagagagacacatctcagaacaacaaatgttccctccacacatgtat 3168
Oy 3241 cagttactgagacatgttatccaagctctatcttaccagccgggaactatccctc 3300
Db 3169 cagttactgagacatgttatccaagctctatcttaccagccgggaactatccctc 3228
Oy 3301 ctttccctaagaacatag 3318
Db 3229 ctttccctaagaacatag 3246

RESULT 3
AAK5514
ID AAK5514 standard; DNA; 3339 BP.
XX
AC AAK5514;
XX
DT 26-JUL-1999 (first entry)
XX
DE Mouse SLO3 (mSLO3) encoding DNA.
XX
KW Voltage-gated; pH sensitive; potassium channel; SLO3; spermatoocyte;
KW sperm capacitation; acrosome reaction; fertilization; infertility;
KW contraceptive; sperm physiology; channel protein; gene therapy; ss.
XX
OS Mus sp.
XX
PN W09920754-A1.
PD 29-APR-1999.
XX
PF 21-OCT-1998; 98WO-US22321.
XX
PR 27-FEB-1998; 98US-0076172.
PR 22-OCT-1997; 97US-0065138.
XX
PA (UNIM) UNIV WASHINGTON.
PI Salkoff L, Schreiber M, Silvia C;
DR WPI: 1999-326593/27.
XX P-PSDB: AAY13437.
XX Voltage-gated, pH-sensitive potassium channel useful in gene therapy
PT Claim 8; Page 77-78; 93pp; English.
XX
CC The invention relates to a voltage-gated, pH sensitive potassium channel
SLO3, expressed in spermatoocytes. SLO3 has, as a monomer, calculated

CC molecular weight 120-156 kD; has unit conductance (as a functional
CC tetramer, when expressed in *Xenopus oocytes*) of 80-120 pS; has increased
CC activity at intracellular pH above about 7.1 and binds specifically to
CC polyclonal antibodies against sequences shown in AAV13437, AAV13438,
CC AAV13442, and AAV13443. S103 is involved in sperm capacitation and/or the
CC acrosome reaction, essential steps in fertilization. S103, and the
CC nucleic acid encoding it, are used to identify specific inhibitors and
CC activators (potentially useful for treating infertility and as
CC contraceptives), also for studying sperm physiology *in vitro*.
CC S103-specific antibodies are used for diagnostic detection of S103
CC expression. S103, as part of a chimera with another channel protein, can
CC be used as a reporter for measuring changes in potassium concentration,
CC current flow, ion flux, etc. Fragments of S103 nucleic acid are useful as
CC probes for identifying homologs, variants and mutants associated with
CC disease; to detect S103-related mRNA or protein; for chromosomal
CC localization; in gene therapy; for identifying potential modulators; to
CC measure up-regulation of S103 in drug screening assays and for production
CC of recombinant S103 protein. The present sequence represents a DNA
CC encoding a mouse S103 (mS103).

XX Sequence 3339 BP; 900 A; 811 C; 734 G; 894 T; 0 other;

Db	661	tcaatgaaagctttccaaactgctgtgtcaataagttacagtaactcgtgttcacgycgacgaga	720
Oy	721	ttcattcacccctggtggaanaattcctgtgtatcccttggtccaaagtagaataatcacagaat	780
Db	721	ttccttcacccctggtggaanaattcctgtgtatcccttggtccaaagtagaataatcacagaat	780
Oy	781	atacatatatttgatgtaatttaccctgtatgagcaaacagtcacacgttgatttga	840
Db	781	atgcataactcttgatctatctatctacctgtgacagcaacaatgccaactgtgtgcttgag	840
Oy	841	gattgtgtagccaagacatcccttagagccgagaccttcatactgtctctacaaacttggagat	900
Db	841	gaatgtgtgtagccaagacatcccttagagccgagaccttcatactgtctctacaaacttggagat	900
Oy	901	tgtatattatttggaactatataccctggaattgttggaactgtgtgtctaaacaaaggaaa	960
Db	901	tgtatattatttggaactatataccctggaattgtgttggaactgtgtgtctaaacaaaggaaa	960
Oy	961	tacaccagtttcmatatgaaagcactcaaaagaaagaatttattgtgtctctgtgaaacatc	1020
Db	961	tacaccagagccctcagaaagcagctcaaaagaaagaagaatttattgtgtctctgtgaaacatc	1020

Query Match	56.0%;	Score 1857;	DB 20;	Length 3339;
Best Local Similarity	74.8%;	Pred. No. 0;		
Matches 2360; Conservative	1;	Mismatches 771;	Indels 21;	Gaps 2;

1021 acagttgacagctgttaactgttcctccgagaaattctctgcacacggaagtcgcgggaaatc 1080

[illegible][illegible]

QY	1601	ttttactggttcagctctgctcaatgtagtctgcttcaattcctctgagctcaatcaactgctgagc	1600
Dp	1798	ttttactggttcctcaactgctccacagctgattctgtctgcaatccctgagctcaattctggaatgctac	1857
QY	1861	tgcacaaagcgaagccgagccgacacatcaagatgccaatctgctgttaagaagatgaataaagt	1920
Dp	1858	tgtcaaaatcaagaagccgacacaacaactccaatagacacgacatcaatgctgattgaagaagcagc	1917
QY	1921	ctgaaaggaatctctctctcgtatatacagggcagagattctctcgcccaagggatct-----	1974
Dp	1918	ttagcagattcaaccactctcttcacacatccacatccagctctctatgttcaacaagaattcaact	1977
QY	1975	-----gaaagcaattcgagcatatacaacttcaaccacacaggaactcttcaacat	2022
Dp	1978	tgtttttcaagaagaaacagacctagtttgtacacacatatacacaacaagacacagacaaac	2037
QY	2023	gagtgaaacaaagatctctgacacgacttgatatacagttggagattttctacatgctgcaaca	2082
Dp	2038	gacacagtgagatgaatacagcaatgctgagacagcagatgagatgttccactctgctgcagaa	2097
QY	2083	acactcttgagacaaggtgaaactctgaaacagaaatctggcaagataaagtcttcogaa	2122
Dp	2098	atgccccttgagacaaggtgctgtctcgaacagagtgaggaagcgaaacacagatctcagaa	2157
QY	2143	caatactgagcatgctgtaatttgagatctgcacatcgccacacagcccgatgggcttcogaa	2202
Dp	2158	cacacttgaaatagctgctgttttgagatgtgcacaaatgtaacctgtgggcttcogaaattc	2217
QY	2203	gtaaatgccccttgagagccaaacactatacacaaggaagagactgtaaagacatagtgtcaat	2262
Dp	2218	gtgagtgccccttgagagagccaaacactatacaccggcagagactgtaaagacatgttttatt	2277
QY	2263	gggctcttgagacactatacacaaggaagatgtagatctctccggaattctcccaagataaac	2322
Dp	2278	gggctcttgagatcaatctccagagagatgtagatctctccggaactctcccaagataaac	2337
QY	2323	atctctgctgtagctgcaattattctctgagacatccatcagctccgaacatagagaatgctc	2382
Dp	2338	atctagccttgagatctcagactctatactgagatgctatgtacgtacatgatagtagagatgctc	2397
QY	2383	tccaatgctgctgtctgtctgtcccccacaccccgacatacgaagaacagaaacttgtagaac	2442
Dp	2398	tctatgtgctgctacatcttaagcacaacactcaacaagagcactgagacagaaatctgtgtgac	2457
QY	2443	acagaagacactcaatgagcaacccctcacacatcggaatcccttcaaatgacatctccctctac	2502
Dp	2458	acagaagacactcaatgagcacaacccctcaacatcccgctccgtcgtgataccaagtctactcca	2517
QY	2503	ccgtcaacccctcagtgctcagaagagagactccgaagtatacacaatatgacataatgagaatca	2562
Dp	2518	gggtctctcaagctcagataaggaagaagcgaatcatctgctcttgtagtgaagaagaaga	2577
QY	2563	aactgcgcgaagaatctccataccttaactgaaactgaaataatctctccacaatccaattatt	2622
Dp	2578	agatacaaaaagatctcccatcttccatactgaaactgaaagaatccctccacaatccaattatt	2637
QY	2623	gaacagatctgtgaaactgagaaaggggtcccccgaagaacaaatctgcatctcgaacgtgccc	2682
Dp	2638	gagcagatctgggcgaactgtagatgctcccaagaaggaactagctgtcaatcccgacactctc	2697
QY	2683	tcttctacgggcacgttcttttccagaagctctcttgaaatctctgctctgctgcgacagccttc	2742
Dp	2698	tcttccacgcggtctgtcttttcagacactctcttggaattctctctctgcgacagccttc	2757
QY	2743	tacaattatcatgtctctggaaattgcttcaagatgctgctgagacagggaggaagtctctcag	2802
Dp	2758	tacaattatcaatgctcgtggaaattactctcagatgctagtgactcggagagacataaagctctcag	2817
QY	2803	ctggaacaacatctagaataaggaataaagctatgctgtgtagagatgactgacgtcgtctc	2862
Dp	2818	atggaacaacatcttggttaagggagaagccctataaagacaactggaagactataagagcaatc	2877

QY	2863	ttgtcctgaagaacccggttaagctcggggctctctcttaacagaaacutttaca	2922
Db	2878	aagctcgtggagacgcgcgtgttaagctcgggacccctctcttaagaccaaacgtttaca	2937
QY	2923	gaagctaacccaagaacacacctttggaacaactgtctcgtgctcatltagatcttttga	2982
Db	2938	ggccttaaccagaanaaacctttggaacgcgtctctcgtgctcatltgataatcttcgg	2997
QY	2983	atccctggttttgcttatccgaataattgtaagaagagagacttaaccggaanaacaa	3042
Db	2998	atccctaaagtgcggtcttatccgttaagatttgatgaagaagaaacccaagacaagaacaa	3057
QY	3043	aagcttcttgatcacccgcgcgaagcacaatlgatctcaagctctgcctcttcagatcttgctt	3102
Db	3058	aagcttcttgatcaccaagcgcatacatgaagtgcacacctcgtgcccttcagatctcgtctt	3117
QY	3103	tgtgcatacccttcagacactcgtctgttataaa	3135
Db	3118	tgtgcatacccttcacaacacactcgttgacaa	3150

RESULT	4
AA5515	
ID	AA5515 standard; DNA; 416 BP.

AC AAX55515

DT 26-JUL-1999 (first entry)

Human SIO3 (hSIO3) encoding DNA.

KM Voltage-gated; pH sensitive; potassium channel; Slo3; spermatocyte
KM sperm capacitation; acrosome reaction; fertilization; infertility;
KM contraceptive; sperm physiology; channel protein; gene therapy; ss

OS Homo sapiens

PN W09920754-A1

PD 29-APR-1999.

PF 21-OCT-1998; 98WO-US22321.

PR 27-FEB-1998; 98US-0076172.

XX

XX XX

XX

DR P-PSDB; AAY13438.

PT Voltage-gated, pH-sensitive potassium channel useful in gene therapy

PS Claim 9; Page 78-79; 93pp; English.

CC The invention relates to a voltage-gated, pH sensitive potassium channel

CC molecular weight 120-156 kD; has unit conductance (as a functional

CC activity at intracellular pH above about 7.1 and binds specifically to

CC AAY13442, and AAY13443. SLO3 is involved in sperm capacitation and/or the

CC nucleic acid encoding it, are used to identify specific inhibitors and

CC contraceptives), also for studying sperm physiology in vitro.

CC expression. Slo3, as part of a chimera with another channel protein, can

CC current flow, ion flux, etc. Fragments of SiO₃ nucleic acid are useful as

AAFS8254/C
ID AAF58254 standard; DNA; 936 BP.
XX
AC AAF58254:
PT
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1875.
XX
KW Electron-transfer group; ETW; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN MO200107665-A2.
PD
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 200OWO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 200OUS-0190259.
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX
XX Umek RM;
PI
DR WPI; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
PT
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETW) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

Query Match	2.88;	Score 94.4;	DB 22;	Length 936;
Best Local Similarity	0.78;	Pred. No. 4.3e-17;		
Matches	5;	Conservative 445;	Mismatches 296;	Indels 0;
			Gaps	0

[illegible][illegible]

RESULT	7
AAFS8257/C	
ID	AAFS8257 standard; DNA; 936 BP.

AC AAF58257;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D1954

KW Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.

OS Synthetic

PN W0200107665-A2.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000WO-US20476

PR 17-MAR-2000; 2000US-0190259

PA (CLIN-) CLINICAL MICRO SENSORS INC

PI Umek RM;

DR WPI; 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface -

PS Example 6; Page 127; 159pp; English.

CC The present invention relates to a composition comprising two nucleic

CC different redox potentials. The invention is used for electronic

CC and single-nucleotide polymorphisms, e.g. for genotyping.

S0 Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

[illegible][illegible]


```
OY 623 aaatctgcaattctacgagccatcaagacagtaactcagtgaaatttccaaactgc 682
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 362
OY 683 tgcataataatctcagtaactcgtgtcacagctgcggagatcaatcactggtggaatt 742
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 422
OY 743 ctggtgatccctgctcaaggttagaatcaacgaatatatatttgatcaattc 802
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 482
OY 803 acctggtcatgcaacaacgctcaacggttgatttgagatggtgagcaagacatcct 862
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 542
OY 863 tagagcagcactcaatcagtctctcacactggggagttgatatatttcggaactata 922
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 602
OY 923 taactgaatggtgtaactgtttgtctaaagaaggaataacacagttcmtatgaagcac 982
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 662
OY 983 tcaagaagaagaagtttatgtgtctgtggaacatcactgtgacagttgacgcctt 1042
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 722
OY 1043 tccgtgagaatttccctcgcgacaaagtcagagagatcaacactgaaattglttcctgg 1102
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 782
OY 1103 gagaaccctcc 1115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 783 wwwwwwgcccccc 795

RESULT 12
AAF58254
ID AAF58254 standard; DNA; 936 BP.
XX
AC AAF58254;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1875.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN W0200107665-A2.
XX
PD 01-FEB-2001.
XX
PE 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface
XX
PS Example 6; Page 127; 159p; English.
```

```
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
```

```
Query Match 2.88; Score 93.4; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 8.3e-17;
Matches 10; Conservative 461; Mismatches 322; Indels 0; Gaps 0;
```

```
OY 323 tttgtctgtctaaagcttgggtctctataatctatcaatctctcgaacctg 382
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 62
OY 383 ttggaagctgtcatcatatgaaagacaacacatccattgatttggtttcaaagtct 442
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 122
OY 443 tcttagttctatcttgataggttattatgacgctgatacagaatcaagttctggc 502
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 182
OY 503 tggagatgaattcaatcgttagacatcttaccatcccaaccttctctatctt 562
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 242
OY 563 tgaagaagcaattgcttaggtttaaagttcctaagaagcttcgcctgtgaaactccctc 622
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 302
OY 623 aaatctgcaattctacgagccatcaagacagtaactcagtgaaatttccaaactgc 682
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 362
OY 683 tgcataataatctcagtaactcgtgtcacagctgcggagatcaatcactggtggaatt 742
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 422
OY 743 ctggtgatccctgctcaaggttagaatcaacgaatatatatttgatcaattc 802
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 482
OY 803 acctggtcatgcaacaacgctcaacggttgatttgagatggtgagcaagacatcct 862
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 542
OY 863 tagagcagcactcaatcagtctctcacactggggagttgatatatttcggaactata 922
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 602
OY 923 taactgaatggtgtaactgtttgtctaaagaaggaataacacagttcmtatgaagcac 982
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 662
OY 983 tcaagaagaagaagtttatgtgtctgtggaacatcactgtgacagttgacgcctt 1042
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 722
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Db 723 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 782
OY 1103 gagaaccctcc 1115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 783 wwwwwwgcccccc 795

RESULT 13
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CC monitoring gene expression.
XX Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 2.88; Score 93.4; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 8.3e-17;
Matches 10; Conservative 461; Mismatches 322; Indels 0; Gaps 0;

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Db 3 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 62

OY 383 ttggaagctgtcatcatatgaagacaaacattcctatgatttggtttcaatgctt 442
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 122

OY 443 tctttagttctattttgatttgagttttagtgagctgataagaatcaagtctgyc 502
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 182

OY 503 tggagatgaattcaatcgttagacatttaccaccacacatttcttctattt 562
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 242

OY 563 tgaagagcaattgcttagtttaagttccttaagaccttgcctgctagaaactcctc 622
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 302

OY 623 aaactctgcaaatcttaagacatcaagaccgaactcagtgaaatttccaaactgc 682
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 362

OY 683 tgtcaataatctcaagtcacccgtgttcaagctcgggagttcaatcactggtgtaaat 742
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Db 363 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 422

OY 743 ctggtgacccctgctcaaggtagaattcacagaatatacatatttgaagcaatt 802
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 482

OY 803 aactgtgcatcgaacaacgltcaacglttgatttgagatgltgtagcaagacatcct 862
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 542

OY 863 tagaagcgaactcatcatgttcttcaacatcgggagttgatatatttcggaacta 922
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 602

OY 923 taactgaatggtggaactgtttgtctaaagaggaatatcacaggtcmtatgaagac 982
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 662

OY 983 tcaagagaaagaagtltatgtgtctgtggaacatcaactgtgagagltgagacgtt 1042
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 722

OY 1043 tctcgtgagaaatttctcctcgacaaagtcagagagatcaacactgaaatttctcctg 1102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 782

OY 1103 gagaacccctcc 1115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 783 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 795
```

RESULT 15
AAFS8262
ID AAF58262 standard; DNA; 936 BP.
XX
AC AAF58262;
XX
DT 24-APR-2001 (first entry)

```
XX 01gongnucleotide D2007.  
DE  
XX Electron-transfer group; ETM; mismatch; genotyping;  
KM gene expression; ss.  
XX  
OS Synthetic.  
XX  
PN WO200107665-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 26-JUL-2000; 2000WO-US20476.  
XX  
PR 26-JUL-1999; 99US-0145695.  
PR 17-MAR-2000; 2000US-0190259.  
XX  
PA (CLIN-) CLINICAL MICRO SENSORS INC.  
XX  
PI Umek RM;  
XX  
DR WPI: 2001-159728/16.  
XX  
PT Nucleic acids containing electron-transfer group, useful as labels in  
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on  
PT a single surface  
XX  
PS Example 6; Page 128; 159pp; English.  
XX  
CC The present invention relates to a composition comprising two nucleic  
CC acids each containing an electron-transfer group (ETM) having  
CC different redox potentials. The invention is used for electronic  
CC detection of nucleic acids, especially of substitutions (mismatches)  
CC and single-nucleotide polymorphisms, e.g. for genotyping.  
CC monitoring gene expression.  
XX  
SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match 2.88; Score 93.4; DB 22; Length 936;  
Best Local Similarity 1.3%; Pred. No. 8.3e-17;  
Matches 10; Conservative 461; Mismatches 322; Indels 0; Gaps 0;



```
OY 323 ttgcttcttaagaatcgtgctcttataatcattatcattcattcgtcgcctg 382
 :
Db 3 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 62

OY 383 ttggaagctgtcatcatatgaagacaaacattcctatgatttggtttcaatgctt 442
 :
Db 63 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 122

OY 443 tctttagttctattttgatttgagttttagtgagctgataagaatcaagtctgyc 502
 :
Db 123 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 182

OY 503 tggagatgaattcaatcgttagacatttaccaccacacatttcttctattt 562
 :
Db 183 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 242

OY 563 tgaagagcaattgcttagtttaagttccttaagaccttgcctgctgtagaaactcctc 622
 :
Db 243 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 302

OY 623 aaactctgcaaatcttaagacatcaagaccgaactcagtgaaatttccaaactgc 682
 :
Db 303 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 362

OY 683 tgtcaataatctcaagtcacccgtgttcaagctcgggagttcaatcactggtgtaaat 742
 :
Db 363 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 422

OY 743 ctggtgacccctgctcaaggtagaattcacagaatatacatatttgaagcaatt 802
 :
Db 423 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 482
```


```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2001, 14:49:10 ; Search time 17859.3 Seconds

(without alignments)
2874.546 Million cell updates/sec

Title: US-09-176-664-17

Perfect score: 3319
Sequence: 1 atgttcagacaagctacg.....tctttcctaagaataag 3319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenDbml:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_om:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_pl1:*
- 13: gb_pl2:*
- 14: gb_pl3:*
- 15: gb_pl4:*
- 16: em_ba1:*
- 17: em_ba2:*
- 18: em_fun:*
- 19: em_htgo_hum:*
- 20: em_htgo_inv:*
- 21: em_htgo_rod:*
- 22: em_htg_hum1:*
- 23: em_htg_hum2:*
- 24: em_htg_hum3:*
- 25: em_htg_hum4:*
- 26: em_htg_hum5:*
- 27: em_htg_hum6:*
- 28: em_htg_hum7:*
- 29: em_htg_hum8:*
- 30: em_htg_inv1:*
- 31: em_htg_inv2:*
- 32: em_htg_other:*
- 33: em_htg_rod:*
- 34: em_hum1:*
- 35: em_hum2:*
- 36: em_hum3:*
- 37: em_hum4:*
- 38: em_hum5:*
- 39: em_hum6:*
- 40: em_hum7:*
- 41: em_in:*
- 42: em_om:*
- 43: em_or:*

- 44: em_ov:*
- 45: em_pat:*
- 46: em_ph:*
- 47: em_pl:*
- 48: em_ro:*
- 49: em_sts:*
- 50: em_sy:*
- 51: em_un:*
- 52: em_vi:*
- 53: gb_sts1:*
- 54: gb_sts2:*
- 55: gb_sts3:*
- 56: gb_sy:*
- 57: gb_un:*
- 58: gb_v11:*
- 59: gb_v12:*
- 60: gb_htg1:*
- 61: gb_htg2:*
- 62: gb_htg3:*
- 63: gb_htg4:*
- 64: gb_htg5:*
- 65: gb_htg6:*
- 66: gb_htg7:*
- 67: gb_htg8:*
- 68: gb_htg9:*
- 69: gb_htg10:*
- 70: gb_htg11:*
- 71: gb_htg12:*
- 72: gb_htg13:*
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- 79: gb_htg20:*
- 80: gb_htg21:*
- 81: gb_htg22:*
- 82: gb_htg23:*
- 83: gb_htg24:*
- 84: gb_htg25:*
- 85: gb_pr1:*
- 86: gb_pr2:*
- 87: gb_pr3:*
- 88: gb_pr4:*
- 89: gb_pr5:*
- 90: gb_pr6:*
- 91: gb_pr7:*
- 92: gb_pr8:*
- 93: gb_pr9:*
- 94: gb_rot1:*
- 95: gb_rot2:*
- 96: gb_in4:*
- 97: gb_pr10:*
- 98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1857	56.0	3339	94	AF039213 Mus muscu
2	705	21.2	3591	94	AF026001 Mus muscu
3	704.2	21.2	3456	88	AF026001 Mus muscu
4	704	21.2	3459	7	AF026000 Sus scrofa
5	697.8	21.0	3364	89	AF118141 Homo sapi
6	697.8	21.0	3537	97	U23767 Human calci
7	697.8	21.0	5829	97	U11058 Homo sapien
8	696.6	21.0	3581	8	AF036626 Trechymys

9	696.2	21.0	3465	88	AF025999	Homo sapi
10	696.2	21.0	3769	97	HS011717	U11717 Human large
11	696.2	21.0	4149	97	HS013913	U13913 Human large
12	691.8	20.8	3500	95	RN093052	U93052 Rattus norv
13	691.2	20.8	3414	8	AF087663	AF087663 Gallus ga
14	689.6	20.8	3968	8	GGU73821	U23821 Gallus gall
15	689.2	20.7	3357	8	GGU73189	U73189 Gallus gall
16	686.6	20.7	3560	8	AF036625	AF036625 Trachemys
17	683.8	20.6	3844	95	RN055995	U55995 Rattus norv
18	679.4	20.5	3962	7	AF231818	AF231818 Oryctolag
19	671.8	20.2	3448	7	BT060105	U60105 Bos taurus
20	668.8	20.2	3480	7	CEU41001	U41001 Canis famli
21	668.2	20.1	3716	7	AB009312	AB009312 Oryctolag
22	658	19.8	5001	94	MF009363	U09363 Mus musculu
23	653.6	19.7	4266	94	AF135265	AF135265 Rattus no
24	651.6	19.6	2931	94	AF083341	AF083341 Rattus no
25	618.8	18.6	3662	8	AF036628	AF036628 Trachemys
26	589	17.7	3494	8	AF086646	AF086646 Trachemys
27	563	17.0	3516	94	AF156674	AF156674 Mus muscu
28	559.6	16.9	4114	7	AF201702	AF201702 Oryctolag
29	558.6	16.8	3755	8	AF036627	AF036627 Trachemys
30	556.2	16.8	5453	95	RN040603	U40603 Rattus norv
31	513.2	15.5	2016	97	HSU09384	U09384 Human calci
32	464	14.0	3090	93	HSU02632	U02632 Human calci
33	379.4	11.4	4232	6	DROSLO	M69053 D.melanog
34	379.4	11.4	4415	6	DROKCHAN	M96840 Drosophila
35	373.8	11.3	2379	8	GGU73823	U23823 Gallus gall
36	252	7.6	100000	91	AP000074	AP000074 Homo sapi
37	196	5.9	100000	91	AP000075	AP000075 Homo sapi
38	188	5.7	62342	78	CEY90453	AC090453 Homo sapi
39	110.4	3.3	110000	83	CEY51A2_2	Continuation (3 of
40	110.4	3.3	139259	6	CEY51A2D	AL021497 Caenorhab
41	109.4	3.3	108433	83	CEY37H2_3	Continuation (4 of
42	96.8	2.9	62342	78	AC090453	Continuation (4 of
43	93.2	2.8	61969	63	AC014103	AC014103 Drosophila
44	93.2	2.8	169271	4	AC009916	AC009916 Drosophila
45	93.2	2.8	256608	5	AE003748	AE003748 Drosophila

ALIGNMENTS

RESULT 1	AF039213	3339 bp	mRNA	ROD	27-OCT-2000
LOCUS	AF039213				
DEFINITION	Mus musculus pH sensitive maxi K+ channel (Slo3) gene, Slo3-1 allele, complete cds.				
ACCESSION	AF039213				
VERSION	AF039213.1	GI:2826754			
KEYWORDS					
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3339)				
AUTHORS	Schreiber,M., Wei,A., Yuan,A., Gaut,J., Saito,M. and Salikoff,I.				
TITLE	Slo3, a novel pH-sensitive K+ channel from mammalian spermatoocytes				
JOURNAL	J. Biol. Chem. 273 (6), 3509-3516 (1998)				
MEDLINE	98123127				
PUBMED	9452476				
REFERENCE	2 (bases 1 to 3339)				
AUTHORS	Salikoff,I., Schreiber,M. and Wei,A.				
TITLE	Direct Submision				
JOURNAL	Submitted (19-DEC-1997) Anatomy & Neurobiology, Washington University School of Medicine, 660 S. Euclid Ave., St. Louis, MO 63110, USA				

FEATURES

source	location/Qualifiers
gene	1..3339
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	/cell_type="spermatoocyte"
	1..3339
	/gene="Slo3"

CDS		/allele="Slo3-1"
		1..3339
		/gene="Slo3"
		/function="possibly involved in fertilization reaction"
		/note="pH sensitive BK channel; abundantly expressed in spermatoocytes"
		/product="1"
		/codon_start=1
		/product="pH sensitive maxi K+ channel"
		/protein_id="AA89742.1"
		/db_xref="GI:2826755"
		/translation="MSQTLIDSLNOKLETETSCIEIOAFILSLATPFGULITFL
		FRILAKSSRMKYVKGRCGLLELFSSRIENPLRIKHPVQRRIEMLSNOTVVG
		QVLEVLIVLISGLVITFTNSMDPVRCSSYEDKLTIGDLSFAFVSFTGLRFAA
		EDKIKLEWENNSIVDIEFTIPPTLSYLKSNWGLRLRLRLLELPKILQILQVIT
		SNYSKLSKLISIVTWFVTAAGFLHLNENSGDPLNRNSQTSYFESILVLTAMST
		VGGDVAATSLGRIFVLPFTGLSLIFAVYIPKPVLSFTFRKYTPRAVAKKFTI
		VGGNITVDSVTAFILNPLHMKSGEINLHAKSEKAKHFOHVIYCVRGADQCTLVGRNFV
		TALKFEDLKVAVNENSAACILIANHFPDLDHDENSIMVLSIKNYIPOTRYITOL
		QSONKVPFLSKIPMDWSAGDNIIDCFALKLGFIAQGLVPLGLCTFTLTLEONQVF
		PKHPWQHFLNGLNKLILTORLSNDFVGMTPPOVSRICFVKNLMLIAIQHKEPFSHC
		CTILNPSQVRLNKDYLGFPIADBSKAVRAEFCNSCHSDVCNPLIGKCNKIKS
		ROOLIAPIVWMSKSLDFTTSSHIHAKSEKAKHFOHVIYCVRGADQCTLVGRNFV
		DDTMDLDSGMFHMCRAMPIDKLVYKSEKAKHFOHVIYCVRGADQCTLVGRNFV
		MLPLASNTYRQELKDIYFISLEIFOREMRPLRNFPRVHIMPSSALYMGILIANVDO
		CSKCVLIATPYKALSSQILVDTEALIMTLINQSLRITSPGSSSKSEKPSAPDSKE
		RKQYKQIPILTELKNSNIHFIEOMGLDMLKGTSLHSTSTGSAVSDPLDEL
		LATSFYNYHVELLOMLVTGSISSSEMYLVKREPYRTDYEAIKSGRTCKGLLS
		HLPSDLVFCALPINTTCGKSDSPFRLKTLTQTRRRHPRGRISISITMPTSPIT
		FQSTYTRREGSLSTTPESILWTR"
BASE COUNT		900 a 811 c 734 g 894 t
ORIGIN		
Query Match		56.0%; Score 1857; DB 94; Length 3339;
Best Local Similarity		74.8%; Pred. No. 0;
Matches 2360; Conservative 1; Mismatches 771; Indels 21; Gaps 2;		
Qy	1	atgttcagactcaagcagaatgaatcgggaagctgcgcaaaatgtcttcgca 60
Db	1	ATGTCTCAACATGCTGATGACGTTTAATCAGAAGAGCTTGACGGAACGTCATGTACA 60
Qy	61	actgaagatcaagcagaatcattctctctccttcttgagccttcattgagcaatc 120
Db	61	ATCGAAATCCAGCGACGCTTCATCTTCCTCGGCGACATCTTCGGGGACATCATC 120
Qy	121	atcctgtgactcctcagcctgcatcgtgagatcgtttaaaaaatgcaaatatcaaga 180
Db	121	ATCTTATTCCTTTTCAGATAGCCTTGAAAGCTCMAAAGTTGGAAATACGTCAGGGG 180
Qy	181	acaagaaattatcttggaactgttcacatcaggtacacatcgtctagaagcattagaagc 240
Db	181	CCAAAGAGACGCTTGGAACATTCCTCATCAGCTGAATACGAGGCAATCCCTTGAGAAA 240
Qy	241	ctcgaactcagggacaatttcgtgatatataagaatgtgcttcagccagacctt 300
Db	241	CTTACTTCATGAGATGATTCGTCAGCGCATCGAAAGCTGCTTTCGACAGACGCTC 300
Qy	301	gtggggcaagtggtggtgacccctgtctgttactaaagcatctgggtccttaataatc 360
Db	301	GTGGGGCAAGTGTGGTATCTTGCTTGTACTAAGCATCGGGTCTTGCTGTATCAT 360
Qy	361	ttcatcaatctgcgtccctcgttggaagcgtgtcatcatatagaagaaaacaatcct 420
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Oy	1021	acgtgtgacaagcttgaaacgccttcctcgaagaaattccctccggaacagtcgaagagatc	1080
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DEFINITION	Mouse mslo mRNA, complete cds.		
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	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Butler,A., Tsunoda,S., McCobb,D.P., Wei,A. and Salkoff,L.		
TITLE	mslo, a complex mouse gene encoding 'maxi' calcium-activated potassium channels		
JOURNAL	Science 261, 221-224 (1993)		
MEDLINE	93318148		
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LOCUS
DEFINITION Macaca mulatta calcium-activated potassium channel alpha subunit

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 AF026001
 AF026001.1 GI:2570857
 KEYWORDS
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 'rhesus monkey.
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 Rae, J.L. and Shepard, A.R.
 Direct Submission
 Submitted (22-sep-1997) Physiology and Biophysics, Mayo Foundation,
 200 1st Street SW, Rochester, MN 55905, USA
 Location/Qualifiers
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Db 2738 ACATCCCATCATCATGACTAGTAATGATGATTAATGTTTCAGTTTGGACCAAGACG 2797
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Oy 2882 gtaagctgggcttctgccttacaagaacatttatacagagcttaatccaagaaca 2941
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Oy 2942 ccttgcgaacatgcttctgtgctcatatagatcttctgaaatcctgtgtgtgctat 3001
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Oy 3056 cccggccagcaatgctcagctgccttcaagatctgtgtgttctgctcacaacct 3115
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Db 3278 t 3278

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RESULT 4
AF026000 3459 bp mRNA MAM 13-DEC-1997
LOCUS AF026000
DEFINITION Sus scrofa calicium-activated potassium channel alpha subunit mRNA, complete cds.
ACCESSION AF026000
VERSION AF026000.1 GI:2570855
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 3459)
Rae,J.L. and Shepard,A.R.
Molecular biology and electrophysiology of calcium-activated
potassium channels from lens epithelium
unpublished
JOURNAL
2 (bases 1 to 3459)
REFERENCE
Rae,J.L. and Shepard,A.R.
Direct Submission
TITLE
Submitted (22-SEP-1997) Physiology and Biophysics, Mayo Foundation,
JOURNAL
200 1st Street SW, Rochester, MN 55905, USA
FEATURES
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1. 3459
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RESULT 5
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LOCUS AF118141 3364 bp mRNA PRI 19-MAY-1999
DEFINITION Homo sapiens BKCA alpha subunit mRNA, complete cds.
ACCESSION AF118141
VERSION AF118141.1 GI:4868123
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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REFERENCE
1 (bases 1 to 3364)
CAIrens,V.R., Aedly,M.R. and Rusch,N.J.
Cloning and Characterization of BKCA Alpha Subunit from Human
Pulmonary Artery
Unpublished
2 (bases 1 to 3364)
CAIrens,V.R., Aedly,M.R. and Rusch,N.J.
Direct Submission
Submitted (04-JAN-1999) Physiology, Medical College of Wisconsin,
8701 Watertown Plank Rd, Milwaukee, WI 53226, USA
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CDS

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BASE COUNT 857 a 851 c 819 g 837 t
ORIGIN
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Query Match 21.0%; Score 697.8; DB 89; Length 3364;
Best Local Similarity 54.7%; Pred. No. 3.5e-186;
Matches 1576; Conservative 1; Mismatches 1238; Indels 66; Gaps 7;
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3164 T 3164

RESULT 6
HSU23767 3537 bp mRNA PRI 15-MAR-1996
LOCUS Human calcium-activated potassium channel (hslo) mRNA, complete cds.
DEFINITION
ACCESSION U23767
VERSION U23767.1 GI:758790
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3537)
AUTHORS McCobb,D.P., Fowler,N.L., Featherstone,T., Linggle,C.J., Salto,M., Krause,J.E. and Salkoff,L.
TITLE A human calcium-activated potassium channel gene expressed in vascular smooth muscle
JOURN. Am. J. Physiol. 269 (3 Pt 2), H767-H777 (1995)
MEDLINE 96024676
REFERENCE 2 (bases 1 to 3537)
AUTHORS Salkoff,L.

TITLE Direct Submission
JOURNAL Submitted (28-MAR-1995) Larry Salkoff, Anatomy and Neurobiology,
Washington University School Medicine, 660 S. Euclid Ave., St.
Louis, MO 63110, USA
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Query Match 21.0%; Score 697.8; DB 97; Length 3537;
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VERSION	U11058.2	GI:7914977	
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JOURNAL		Wallner,M., Meera,P., Ottolia,M., Kaczorowski,G.J., Latorre,R., Garcia,M.L., Stefani,E. and Toro,L.	
MEDLINE		Characterization of and modulation by a beta-subunit of a human maxi Kca channel cloned from myometrium	
PUBMED		Recept. Channels 3 (3), 185-199 (1995)	
REFERENCE		96419007	
AUTHORS		8821792	
TITLE		2 (bases 1 to 5829)	
JOURNAL		Wallner,M., Meera,P. and Toro,L.	
MEDLINE		Determinant for beta-subunit regulation in high-conductance voltage-activated and Ca(2+)-sensitive K ⁺ channels: an additional transmembrane region at the N terminus	
PUBMED		Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14922-14927 (1996)	
REFERENCE		97121491	
AUTHORS		8962157	
TITLE		3 (bases 1 to 5829)	
JOURNAL		Meera,P., Wallner,M., Song,M. and Toro,L.	
MEDLINE		Large conductance voltage- and calcium-dependent K ⁺ channel, a distinct member of voltage-dependent ion channels with seven N-terminal transmembrane segments (S0-S6), an extracellular N terminus, and an intracellular (S9-S10) C terminus	
PUBMED		Proc. Natl. Acad. Sci. U.S.A. 94 (25), 14066-14071 (1997)	
REFERENCE		96804561	
AUTHORS		9391153	
TITLE		4 (bases 1 to 3987)	
JOURNAL		Wallner,M.	
MEDLINE		Direct Submission	
PUBMED		Submitted (21-JUN-1994) Molecular Physiology and Biophysics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
REFERENCE		5 (bases 1 to 5829)	

REMARK COMMENT FEATURES	JOURNAL	AUTHORS	TITLE
On May 17, 2000 this sequence version replaced g1:507921.	Submitted (17-MAY-2000)	Walther M.	Direct Submission
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RESULT 8
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 alternatively spliced thc3 isoform, complete cds.

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ACCESSION AF036626
VERSION AF036626.1 GI:3136119
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QY	2982	aatcctgctgttggtcctataccggaatatgtgaagaagaagaccacaacc-----aga	3035
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ACCESSION	AF025999		
VERSION	AF025999.1	GI:2570853	
KEYWORDS			
SOURCE			
ORGANISM		human.	
REFERENCE		Homo sapiens	
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
JOURNAL		Rae, J.L. and Shepard, A.R.	
TITLE		Identification of potassium channels in human lens epithelium (in)	
REFERENCE		Civan, M.M. (Ed.);	
AUTHORS		THE EYE'S AQUEDUS HUMOR: FROM SECRETION TO GLAUCOMA: 69-104;	
TITLE		Academic Press, San Diego, CA, USA (1998) In press	
REFERENCE		Rae, J.L. and Shepard, A.R.	
AUTHORS		Molecular biology and electrophysiology of calcium-activated potassium channels from lens epithelium	
JOURNAL		Unpublished	
REFERENCE		3 (bases 1 to 3465)	
AUTHORS		Rae, J.L. and Shepard, A.R.	
TITLE		Direct Submission	
JOURNAL		Submitted (22-SEP-1997) Physiology and Biophysics, Mayo Foundation,	
FEATURES		200 1st Street SW, Rochester, MN 55905, USA	
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		/note="Maxik alpha subunit"	
CDS			

	BASE COUNT	872 a	900 c	828 g	865 t	
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QY 338	gcaatggagctctataatactatctatcaatctcgtcagccctgttggaagctg	394				
DB 491	GCATCGGCGCACTTGATATACCTTCAAGATTCAAGATTCAAAACCAATAGAACCTGCCAGA	550				
QY 395	catcatagaagaacaaacctctcatctatggtttggtttcaagctctttagttct	454				
DB 551	ATTCTCTACAAAGATTTCACATTAACGATCGACATGGCTTTCACAGCTGTTCTTCCCTCTCT	610				
QY 455	attctgagcttgagcttctagcagcttgaagcaagcttcctcgtcttgagatgaat	514				
DB 611	ACTTCGCGCTCGGGTTTATTCGACGCAACGATTAATGTTGGTTCGCTCGGAAGTCACT	670				
QY 515	caatcgtagaacatcttaccatcccaaccaaccttattcttctatatttgaaggaatt	574				
DB 671	CTGTAGTGGATTTCCTACGGGTGCCCGCGTGGTTGTCTGTGTACTTAACACATAATT	730				
QY 575	ggctaggtttaagttctcctaagagcctctgcgccttgtagaactccctcaaatcttgcaa	634				
DB 731	GGCTTGATTGAGATTTTAAAGAGCTGTGAGACGTGATACAGTTTTCAGAAATTTTGCAGT	790				
QY 635	ttctcagagcaatcaagccagtaactcagtggaagtttccaaactgctgtcataaatc	694				
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DB 851	TCAGACAGCTGGCTGACTGACAGCGGGTTCAATCCATTGGTGGAGAAATTCAGGGAGCCAT	910				
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OY	995	agtttatctggtctctgtgaaacaactcgttggacagtgtgaacgcttctcaggaa	1054
Db	1151	AGCAGATTGTGGTCTGGGACATCACTCTGGAGAGTGTTCCAACTCTCGAAGGACT	1210
OY	1055	tcaccgcgaacaagtcagggagatcaacaactgaatcttcttcctcgggagaaaccctc	1114
Db	1211	TTTCGCAACAGACCGGGATGAGCTCATATGGAATCTGTTTTCTTCACAACTCTCC	1270
OY	1115	ctctcttggaaacttgaaacatatcttaatgctacttggcctacaacaacttcatctc	1174
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OY	1175	gattctgcaatgaagtggggagatctcgaagcgagttcggttgaatctctgaaggacatgc	1234
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OY	1235	tgatataagcccaatcctcttgcagagatctccatgctgaagatatcttcaacatitga	1294
Db	1391	TGATGCTTGCCACAACTACTGGCGTGACCCGGATGCGGAGGATCGCTGAAATATCATGA	1450
OY	1295	gggtgctctctatcaagaactatgatctctacacagaatcatcacagatcatgtcaat	1354
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OY	1355	cccaatacaaggttatctctgcgaagaatcccaagctcggaaactcgggaacccggagca	1414
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OY	1415	tcaatcgtcttgcgtgaattaaacttgaattatctgcaccaagcgctgttgtgtccagct	1474
Db	1571	CAATCTGCTGCGAGAGTTGAAGTTGAGTGGGCTTATACCCAGAGCTGCGCTCAAGGCC	1630
OY	1475	tgttgatcttcctcaactctctctcttcttggagagaaacaaaagttatgctctaacga	1534
Db	1631	TCTCCACCATGCTTGGCCCAACCTCTCTCCATGAGGCTCATTTCAAAAGATTGAGTAAGCA	1690
OY	1535	ccgtggaagaaacactctcttgaatagatgaaagaaacaaatctctgaccccaacgctctctg	1594
Db	1691	CATGGCAGAAATACTACTTGTGAAGGAGTCCAAATGAATGTAACAAGAAATATCTGCCA	1750
OY	1595	atgacttgcgtgaaatgaagcttccctggaagtgtgccgcgtctcgtcttctgaaatgtacc	1654
Db	1751	GTGCTTCTGTTGGGCTCTCTCTCTCCCTCAATGTTTGTAGCTGTGTTTGTGAAGCTCAAGC	1810
OY	1655	tcctgttgaatgacatcgaaatacaagtcctcttcaaggatgttctctgtgtgcgtatc	1714
Db	1811	TCTCAATGATATGATCATGTGATACAGTC-----TCCCAACGAGAGAGCCCTATATATTA	1864
OY	1715	taaatccaactccaagaatgaagatacgtatagaacaacatlaaggtctcttatgtctgaa	1774
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OY	1775	ctcgaagaagcgtctagaaggccttgttcttactcgttcagtcgtcatgatgtgtgttca	1834
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Db	2287	T	GAGTGGCGCATGTGTGGTGTGGATCTTTTGGGACGCTCAGCTCAGCTCGATCGGCGCTCC	2328
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OY	2702	t	tttcacgaagcttctctgaaatctctctgcgtgcgagcctctctacaatatacagttccg	2761
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DEFINITION			PRT
			28-JAN-1996
			Human calcium activated potassium channel (hsio) mRNA, complete cds.
ACCESSION	U11717		
VERSION	U11717.1	GI:606875	
KEYWORDS			
SOURCE			human.
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS			1 (bases 1 to 3769)
TITLE			Tseng-Crank,J., Foster,C.D., Krause,J.D., Mertz,R., Godinot,N., DClhara,T.J., and Reinhardt,P.H.
JOURNAL			Cloning, expression, and distribution of functionally distinct
MEDLINE			Ca(2+)-activated K+ channel isoforms from human brain
REFERENCE			Neuron 13 (6), 1315-1330 (1994)
AUTHORS			95085775
JOURNAL			2 (bases 1 to 3769)
TITLE			Tseng-Crank,J.
REFERENCE			Direct Submission
AUTHORS			Submitted (30-JUN-1994) Julie Tseng-Crank, Molecular Genetics,
JOURNAL			Glaxo Research Institute, 5 Moore Drive, Research Triangle Park,
FEATURES			27709, USA
source			Location/Qualifiers
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QY	755	ggctcaagaagtagaaatctcaacagaaatactatcttcttgaagcaatttaccggtgcacg	814		
DB	935	GGGAAATTTCCAAANACAACAGCGCTCTACCTACTGGGAATGTCTTATTTACTCATGG	994		
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 1955 attctccgcaaggtatctgcgaagcactcgaacatatacaacttcaacacagagctc 2014
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 2591 TGCAGACAAAGAAATGCATCTGTGGCGTCACTCAACATCAATGATGATGATGATGACA 2650
 2494 -----tccctgaacccgtcaacccctgaatgataagagagactccaggt 2536
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 2711 CTCAGATTAACAGCCCGTGCAGGGATGTTTACTCAACATCATCATCAACTGGGGTCA 2770
 2597 aaatccttccaaacatcacttattatgaacagcttggtagactggaaggtccccc----- 2650
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 2822 aggaataagctatggtgtgacgaatagctgcacgctcgtcgtcgtcgtggaagaacgggt 2881
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 3116 t 3116
 3311 T 3311

RESULT 11
 LOCUS HSU13913
 DEFINITION Human large-conductance calcium-activated potassium channel (hsl10)
 ACCESSION U13913
 VERSION U13913.1 GI:537438
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 79 to 3615)
 REFERENCE Dwoiretzky,S.I., trojnakl,J.T. and Gribkoff,V.K.

[illegible]

OY	455	attctggaattgaagttctgaigcgaactggaagcaagatcgaagttctgcgcggaggaattgaatt	51
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OY	515	caatcgtgaacatctcttaccatcccaaccaacttlatctctatctcttgaagagcaact	574
Db	821	CTGTAGTGGATTTCTTCACGGGTGCCCGGTGGTTGGTGTGTGACTTAAACAGAGTT	880
OY	575	ggcctgaagtctaaagttccctaaagcctctgcgcctgtctagaactccctcaactctgcaaa	634
Db	881	GGCTTTGGTTTGAAGATTTTTTAAAGACCTCTGGAGCTGTATACGTTTTCAGAAATTTTGGCACT	940
OY	635	cttcaacgagcaatcaagaaccagaaactcagtggaattcttccaaactgcgcgtcaaatc	694
Db	941	TTTCGAATATTTCTTAAACAAGTAATTCATCAAGCTGGTGAATCTGCTCTCCATATTTA	1000
OY	695	tcagtaacctgtgttcacagctgcggatcatcaacctgylbgaaaaatctcylglatccct	754
Db	1001	TCAGACCTGGCTGACTGACGACGCCGGGTTCATCCATTGGTGGAGAAATTCAAGGGAGCCCAT	1060
OY	755	ggctcaagaagtagaagaattcaacagaatatatcatatttggctcaacttcccggtctacg	814
Db	1061	GGGAAATTTTCCAAANACCAACAGGCTCTCACCTTACCTGGGAATGTGCTATTATCATATGG	1120
OY	815	caacaacgtlcaacacgcttggatttggagaatgttggtaacgaacatcccttaaggacgacct	874
Db	1121	TCACAAATGCTCCACCGCTTGGTGTATGGGATGTTTATGCAAAAACACACTTTGGCGCCCTCT	1180
OY	875	tcaatcagttcttcaacactcggggaagtttgaatatatttcggaactataactgaatgaag	934
Db	1181	TCATAGGTCTTCTTCAATCCTCGGGGGATGGCCATGTGTTGCCACTCTACGTCCCTCGAATATA	1240
OY	935	tggaaactgtctgtcacaagaagagaaacacacacagttcmtatgaagcaatccaagaagaa	994
Db	1241	TAGAGTTAATAGGAACCGCAAGAAATACGGGGGCTCCTTATCGCGTTTATGTGAAGAA	1300
OY	995	agttatctgtggtctgttggaaacatcaactcgttvgacagtlybaccgcgttcccttgaagaa	1050
Db	1301	AGCACATTTGTGTGTGGGGACACATCACTCTGGAGAGTGTTCACACTTCTCTAAAGACT	1360
OY	1055	tcctcccggaagaagtcgaagagaagtaaacactgaatttgtttccctcgggagaagaacccctc	1110
Db	1361	TTTGTGCACAAAGACCGGGAGTACCTCAATGTGGAGATCGTTTTTCTTCACACATCTCC	1420
OY	1115	cttctcttggaaacttggaaacatctttaaactgtcacttgcgtcctacaacagttcattctcg	1170
Db	1421	CCAACTCTGGACTTGAAGCTGTGTTCAACAGACATTTTACTCAGGTGGAAATTTTATACAG	1480
OY	1175	gactctgcaatgaagttgggagagatctgaagcgaagttcgcgttggaaactctgcaaggaatgcc	1230
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OY	1235	tgaatatagcaaatcccttggagagagatcccaactgcgttgaagatatttccaaactaaga	1290
Db	1541	TGATCTTGGCCAAACAAGTACTGCTCCTTACCCTGGATGCGGAGATGCTCTCAATATCATTA	1600
OY	1295	gggtgctctctatcaagaactatgaattctacacacgaagatcatalcatatcagaatactgcaat	1350
Db	1601	GAGTATATTCATTAAGAACTTACCATCCGAAGATTAAGAATCATTCACATCAATGCTCAGT	1660
OY	1355	cccaataaagaagttatctgcgcaagaagttcccaagcttggaaacttggacaaccggaacaaca	1410
Db	1661	ATCCACAAACAAAGCCCATCTGTCTTAAACATCCCGAGCTGGAATTTGAAAGAAGTGATGACG	1720
OY	1415	tcaatctgcttgcgtgaatctaaacttggatttctacgcgcaagacgttgttggltccagagct	1470
Db	1721	CAATCTGCTGCGCAGAGTGAAGTTGGGGCTTATAGCCCAAGACCTCGCTGGCTCAAGGCC	1780
OY	1475	tgtgtaccttccatacatctctatttggtagagcaaaaagaaggtatagcctaaacaga	1530
Db	1781	TCTCCACCATCTCTTGGCAACCTCTTCTTCATGAGGTCATTTCATTAAGAAGTTGACGAAGACA	1840

Oy	1535	ccttgaagaacaaacctcttcgtatgacatgtaaaaaacaattctgcaccaagcgtctcttg	1594
Db	1841	CATGGCAGAAATACTACTTGGAAGAGACTCTCAATTGAAATGTACACAGAAATATCTTCGA	1900
Oy	1595	atgaacttgcgtgaagtagactttccctgaagtctgccggctctcgctcttcctgaagatgaacc	1654
Db	1901	GTCGCTTTCTGGGGGCTCTCTCCCTACTGCTGTTTGAGCTCTGTTTGTGTAAGCTCAAGC	1960
Oy	1655	tcccgtctgatagcaatcgaatatcaaacgccccctttaaggatggtttctgtctgtgttac	1714
Db	1961	TCCCATATGATTAAGCCATTGAGTAGCAAGTC-----TGCCAACCGAGAGACCCTTATATTA	2014
Oy	1715	taaatccacctcccaagtgaggaataagtaagaacacattatggtttcttcatctgtgaaa	1774
Db	2015	TTAATCTGGAAACCATCTTAAGATCCAAGAAGGTACTTTAGATTTTTTCATCCCAAGTG	2074
Oy	1775	ctccaagaagacgtcagaagaagccttgttttaactgtcagttctgcatacatgatatgtgttca	1834
Db	2075	ATGCCAAAGAAAGTTAAAGGGCATTTTTTTTATCTCAAGGCTCTGCATGATGACATCAAG	2134
Oy	1835	ttacctgactaatatcacaaactgtgtcgtcgcacaaagcaagaagccgycacacatacgaatgc	1894
Db	2135	ATCCCAAAGAAATTAATAAATATGTGGCTGCAACGCGTTGAAGATGACACAGCCGTCAACAC	2194
Oy	1895	catctgttaaagaagatgaataaaaatgctctgaaggaaatctccctcgtatatcagggcagg	1954
Db	2195	TATTCACCAAAAAAAAAG-----CAACGGAAATGAGAGCGATGCGGAATCACCCAA	2243
Oy	1955	attctccgaagagtatctgcagaagacttcgagcatatacaattcacccaagagactc	2014
Db	2244	CACCTGCCCTTAAGCTGATGAGGCTAGACCCCTTGTATTTCTCTGGCAATGATCAATG-	2302
Oy	2015	ttcaacatgatlgtagaacaaagatctgcagcaagctltgalagatggtgaatgtltaactggt	2074
Db	2303	-----ACAACATGTGACTCCAAATGTGAAAGATGACGACTACTGAGGATGTTTCACTGCT	2356
Oy	2075	gcaaaccaaacctctcttgcagaagtgactctgcagaagaaactgcggaagtccaagtataagt	2134
Db	2357	GTCGACCCCAAGAGATTAAGAAAGTCACTCTGACTCCAAATGGAAGCTGCCATGACGCTCC	2416
Oy	2135	ttcggaaacatltgtagcatgtgtatlttggagaatgccactcaagcccccgtatvggtctc	2194
Db	2417	TGAGTGCCCATATGTCGTGTGCTATCTTTGGCGAGCTCACTCTAGCCCTGATCGGCTCC	2476
Oy	2195	ggaaacttgttaabgtcccttgaagccgagcaactataccagaagaaactgaagaactatag	2254
Db	2477	GGAACTCTGGATGATGCCCTCGGTCGACGACAACTTCAATTACCATGAGACTCAAGCAATTG	2536
Oy	2255	tgctcatctggctctctgagcatatctaagaagaaatgacgaatctctccggaatttccccc	2314
Db	2537	TGTTTTGGGGCTCTAATGAGACTCAAGGGGAATGGAGAGCTTCAATACCTTCCCAC	2596
Oy	2215	agatatacatcttgcctcgtgatgtgcactttaactcttgcagaactcccatcgtgcgaactag	2374
Db	2597	AAGTGTCAAATTTGCCGTGACGCAATTAAGTCGGGCTGATTTAAAGGGCTGTCAACATCA	2656
Oy	2375	agcaatgtccatcatgtgtcgtctctgtcccccccaaccgagccatcaagaacaagactc	2434
Db	2657	ACCTCTGTGACATGTGGGTTATCTCTGTGCAGCAATCAAGAAATATATGATGATACTTCCG	2716
Oy	2435	ttgltagagacagaagaacatcatgagcaaccctacacatcgtgatactcttgcaaattgactcc-	2493
Db	2717	TGCAGAGCACAGAAATGATCTTGGCGCTCACTCAACATCAATCTATGACAGTTGATGACA	2776
Oy	2494	-----tctctgaccccgatcaacccttaagtgtctagaagaaatcctcaagtt	2536
Db	2777	GCATCGGAGTCTTGCAGGCTTAATTTCCCAAGGGTTCCACACTCCAGAGAAATGATAGACTCT	2836
Oy	2537	acaacaaatgagacataatgagaaatcaaaactgcgcgaagaagcccatcttactgaactga	2596
Db	2837	CTCCAGATTAACAGCCCAAGTCCAGGGGATGTTACTGTCAACCATCATCAACAATCTGGGTCA	2896
Oy	2597	aaaatccttcaaacatcactttatttgaacagacttggltgacttgaagaygtctcc-----	2650

Db	2897	ACATCCCATCATCTACTGAGTGAACGAACTAATGTTCAGTTTTTGACCAAGAAGC	2956
Oy	2651	-----tccaagaacaacatctgcalctcagcaactgtccctttctaogggcacgtttc	2701
Db	2957	ATGATGATGACCCTGATACAGAACTGTAACCTCACCAACCCCCTTTGCGTGAGACGAT	3016
Oy	2702	tttccgaagcttccttgatctctgcgcggcgacggccttcaaatataatcgtcctg	2761
Db	3017	TTCGGCTAGTGTCTCGACATCACTCATGAGCGGACGACTATTCAATAGACATATCTCA	3076
Oy	2762	aattgctccagatgcctggtgacaaggaggaagtctccagctggaacaacattaga ta	2821
Db	3077	CCCTGATACGAGACCTCGGTGTGACCGGAGGAGGCACGCCGAGAGCTGGAGGCTGTGATTGCTG	3136
Oy	2822	aggataaagctatgtgtgtgcagataagctgcagctgcctctgtctcgtgaagaaccgct	2881
Db	3137	AGGAATAAGCCCTTAGAGAGGTGGCTACACACCCCCCAACAACACTGGCAATAGGGACCGCT	3196
Oy	2882	gtaagctggggcttcctgccttacacagaacacattttaacagctlaataccaagaasaca	2941
Db	3197	GCCGCTGGCCOAGTTACTCTGCTCGATGAGGCCATTGGCGACTTTAGGGAGTGTGGTT	3256
Oy	2942	ccttggaacaactgtctcgtgtgacctaatagatccttttggaaacctgtgttgtctat	3001
Db	3257	GTTATGGAGATCTGTTCGCAAAAGCTTCGAAMAACATATAATATGCTTTGTTGGAAATTT	3316
Oy	3002	accgaatatgatgaagaaggagcaccacccagaanaac-----aaaagutttgatca	3055
Db	3317	ACCGCTAGAGATGCTCACTCAACACACCCAGTCATGCAAAAAGAGATATGCAATCA	3376
Oy	3056	ccccgccagcaatgagltcaagctgtcgtcccttcagatcctgtgttcttgccalaccct	3115
Db	3377	CCAACCCCCCTATGAGTGTAGCTCGTCCGACGACGAGACCTATCTTCGCTTAATGACAGT	3436
Oy	3116	t 3116	
Db	3437	T 3437	
RESULT 12			
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LOCUS	RNU3052	3500 bp	mRNA
DEFINITION	Rattus norvegicus calcium-activated potassium channel alpha subunit		
VERSION	U93052		
KEYWORDS	U93052.1 GI:1929017		
SOURCE	Norway rat.		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
TITLE	Rattus.		
JOURNAL	1 (bases 1 to 3500)		
REFERENCE	Liu,Y., Pleyte,K.A. and Rusch,N.J.		
AUTHORS	Calcium-activated potassium channel alpha subunit from rat aortic		
TITLE	smooth muscle		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3500)		
AUTHORS	Liu,Y., Pleyte,K.A. and Rusch,N.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-MAR-1997) Physiology, Medical College of Wisconsin,		
FEATURES	8701 Watertown Plank Road, Milwaukee, WI 53226, USA		
SOURCE	location/Qualifiers		
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	subunit"		

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OY	2070	ctgtgtcaaaccaaacctctcttgacaagtgactctgaacgaactcgtgaagtcacaagta	2129
DB	2195	CTGGGCGCCACCACCAAGAGATTTGAGAAAGCATCTTGACTCGAAGTAAAGTCGCATGAC	2254
OY	2130	taagttctggagaacacatttgtagatgtagatttggaatgtcccaactgaagccccaatgg	2189
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OY	2190	gcttcggaactctgtaagtcgaccttgagagccgaacataacagaagaagatctgaaga	2249
DB	2315	CCTCGGAAACCTGGTGAATGGCGGCTTGCTGTACCAATTTTCACTATCAGATGACTAAACA	2374
OY	2250	catagtctcatcttggtctctgtgaactatctacaagagaatggcgaattcttcggaattc	2309
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OY	2310	tcaccaagatacaatctctgccttgagatgtgaacttaattctggagacctccatggcgcaa	2369
DB	2435	CCCCAAAGTATTCATATTGCTGTGTACGCCATTAACTGGCGCTGATTTAAGGCGTGTAA	2494
OY	2370	catagagaatgctcccatctgtgtctgtcttcccccaccccaaccgaacatacaagaacca	2429
DB	2495	CATCAACCTCTGTGACATGTGGCTTATCTGTGAGCAATCAAGAAATATATGATGATAC	2554
OY	2430	gaacttgtgaacacagaaagacatcatatgacaaacctccacatcgatctctgcaaatga	2489
DB	2555	TTTGGCTTAGAGACAAAGAAATGCAATCTTTGGGGTACATCAATCAATATATGCAATTTGA	2614
OY	2490	ctccctccctgaaccgcgcacacctgaatgtcagaaggagactccaagtttaacaacatggaca	2549
DB	2615	TGACAGCATCTGGGGTCTTGACAGCTAATTTCCAAAG-GAATTACACCTCTTGGAATGACA	2673
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OY	2610	catctacttaattgaaacagcttgtgtgaactcgtgaaggctc-----	2649
DB	2734	GAGTCAACATTTCCCATCATCAGCAAGAACTCTGAAACATATGTTGAGTTTGGACC	2793
OY	2650	-----ctcacaagaacaactctgaatctctgaacagctctcttcttaacggaca	2695
DB	2794	AAGAGATGATGATGACCCCTGACACAGAGCTGTAACCTCAACAGCCCTTGTGTTGGGA	2853
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DB	2854	CAGCATTTTGGCGGTACAGGCTCTGACATCACTATGAGCCGCAATATCTTCATGACATA	2913
OY	2756	tccttggaaatcttcagatgctcgtgtgacaggaagaaatgaattctcaactcgtgaacaact	2815
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OY	2816	tagataaagataaagactatactgctgtgcagatagatctgcacgctcgtctgtcttgaaaga	2875
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OY	2876	accggtgtlaagctcgtggctctctgtccttacaagaaacatttatacgaagcttaatccaa	2935
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OY	2936	gaacaaccttggacaacactgtctgtgtcattatgaactcttttggaaatcctgtgtgtg	2995
DB	3094	GTGTGTTTATGATGATCTGCTTCTGCAAAAGCTTGAAAAATATATAACATGCTTTGTTTG	3153
OY	2996	gcttatccgaataatgtgaagaagagatctcaacccgaaaaac-----aaaggttg	3049
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QY	3050	tgatcacccggcagcaatggcttcaagcgctcgtccctccagactctgttttgcga	3109
Db	3214	TCATCAGCAATCCCCCTCAGAGCTTTGAACCTGTACCGACAGACTGATCTTTCGCTTGA	3273
QY	3110	taacctt	3116
Db	3274	TCCAGTT	3280
RESULT	13		
LOCUS	AF087663	3414 bp	mRNA
DEFINITION	Gallus gallus calcium-activated potassium channel alpha subunit		
ACCESSION	AF087663		
VERSION	AF087663.1	GI:3599522	
KEYWORDS	Chicken.		
SOURCE	Gallus gallus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
REFERENCE	1 (bases 1 to 3414)		
AUTHORS	Rae,J.L. and Shepard,A.R.		
TITLE	Molecular biology and electrophysiology of calcium-activated potassium channels from lens epithelium		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3414)		
AUTHORS	Rae,J.L. and Shepard,A.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-AUG-1998) Physiology, Mayo Foundation, 200 1st Street SW, Rochester, MN 55905, USA		
FEATURES	Location/Qualifiers		
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